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Scoring table:
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Listing first 45 summaries
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October 12, 2000, 17:23:38 ; Search time 17897.3 Seconds (without alignments) 587.637 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

000	Result No.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2483)
2agon, I.S., Verderame, M.F., Allen, S.S. and McLaughlin, P.J.
Cloning, sequencing, chromosomal location, and function of cDNAs encoding an opioid growth factor receptor (OGFr) in humans
Brain Res. 856 (1-2), 75-83 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF172453 2483 bp
Homo sapiens opioid gi
AF172453
AF172453.1 GI:7595306
                                                                                                                                                                                                                                     Submitted (26-JUL-1999) Department
Pennsylvania State University Colle
Drive, Hershey, PA 17033, USA
Location/Qualifiers
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College of Medicine, 500 University
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M29385 Herpes simp
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2 (agon, I.S., Verderame, M.F., Allen, S.S. a Direct Submission
Submitted (26-JUL-1999) Department of Ne Pennsylvania State University College of Drive, Hershey, PA 17033, USA Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2423)
2agon,I.S., Verderame,M.F., Allen,S.S. and McLaughlin,P.J.
Cloning, sequencing, chromosomal location, and function of
encoding an opioid growth factor receptor (OGFr) in humans
Brain Res. 856 (1-2), 75-83 (2000)
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                                                     Liu,J., Brewton,R.G., Takanosu,M., Direct Submission Submitted (23-NOV-1998) Cell Biolog Birmingham, 1670 University Blvd. V 35294, USA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
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FRPRCKFVWGPQDKLRRFKPSSLPHPLEGSRKVBEEGSPGDPDHEASTQGRTGGPEHS
KGGGRVDEGPQSASEVEKIALNLEGCALSQGSLRTGTQFVGGODPGEAVQPCKQFLGARV
ADKVRKRKVDEGAGDSAAVASGGAQTLALAGSPAPSGHFKAGHSENGVEEDTEGRTG
PREGTPGSPGAFAGDSPAGDDFAESPSETPGGPRAGPAGDEPAESPSETPGPRA
ADKVRKRKVDEGAGDSAAVASGGAQTLALAGSPAPSGHFKAGHSENGVEEDTEGRTG
PREGTPGSPSAGPAGDDEPAESPSETPGPRPAGPAGDEPAESPSETPGPRA
ADKVRKRRKVDEGAGDSPAGPTRDEPAESPSETPGPRPAGPAGDEPAESPSETPGPRA
PAGPAGDEPAKTSETPGPSPAGPTRDEPAESPSETPGPRPAGPAGDEPAESPSETPGPR
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Zagon, I.S., Verderame, M.F., Allen, S.S. and McLaughlin, P.J. Cloning, sequencing, chromosomal location, and function of encoding an opicid growth factor receptor (OGFr) in humans Brain Res. 856 (1-2), 75-83 (2000)
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/db_xref="taxon:9606"
/chromosome="20"
/map="20q13.3"
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requests: clonerequestisanger.ac.uk
On Jul 8, 2000 this sequence version replaced g1:8919619.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
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                                                                                                                                                                                                                Submitted (09-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                               Smith
                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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             /note="4
5051. .51
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4264.

"38 copies .5163 .5159

.5152

5 copies

60 24

'17 copies 51 .5171

mer 59% mer 61% mer 61%

/note=" note-"1

4248.

'note="

4240.

.5151

/note="234 copies 4 mer tccc 60% conserved"

copies 2 mer cc 59% conserved

copies 48 mer 61% conserved"

/note="443 | 4231. .5166

4198. .5157
/note="12 copies 80 mer 61% conserved"
complement(4223. .5153)

LlMA9 repeat: matches 6254. .6302

of consensus"

/note="Tandem repeat. region contains two forced joins single clone. Assembly consistent with restriction

354. .397 /note-"L11

/note="L1MA9 repeat: matches 6210. .6254 of consensus" 65. .353 /note="AluJo repeat: matches 1. .287 of consensus"

/clone_lib-"RPCI-5"

4530. 4486

.5087 .4822

74

mer 69% conserved"

. 5151

copies

33 mer

803 809 809

.5148

34 19

mer mer mer

5144

12 copies

.5145

copies 47

59% conserved"

conserved" conserved"

conserved" conserved" conserved" conserved" conserved'

"2/ copies .5156

32

mer 61%

'note="] /note- "9

.8 copies 31 mer 71% conserved

58

mer

778

conserved"

="11 copies 38 .5064 - 5 copies .5137

mer 61% conserved

copies 58 mer 79% conserved

copies

σ

tctctc 63% conserved"

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feature key.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                         This sequence is the entire insert of clone RP5-885L7 The true left end of clone RP4-563E14 is at 140192 in this sequence. The true right end of clone RP11-93B14 is at 44512 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                      http://www.sanger.ac.uk/HGP/Chr20

RP5-885L7 is from the library RPCI-5 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For furth details see http://bacpac.med.buffalo.edu/

VECTOR: pCYPAC2
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="20"
/map="q13.2-13.33"
/clone="RP5-885L7"
                                                                                                                                                                                                     1. .16024
                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                      de Jong. For further
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consensus"

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60;

Gaps

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/note="LIM4 repeat: I
6974. .7049
/note="4 copies 19 mo
7224. .7451
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18307. .1
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                                                         /note="8 |
18497. .1
                                                                                                                /note="11 copies 16 18325. .18486
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18321. .18496
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/note="5 copie
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15824. 15891
/note="17 copies 4 mer tccc 67% conserved"
16266. 16577
/note="AluSq repeat: matches 1. .313 of co
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/note="11 copies 24 mer 68%
16582..16891
/note="10 copies 31 mer 66%
                                /note="25 copies 2 mer
19329. .19433
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/note="Alur repeat: matches 5.
|0876. .10962
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'note="10 copies 4 mer
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| 16848. .16899
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11974. .12025
                                                                                                                                                                                319. 18486
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98. .16837

.em"5 copies 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                           e="3 copies 80 mer 77% conserved"
8. .16901
e="44 copies 6 mer aaagaa 62% conserved"
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5. .16840
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                                                                                    "9 copies 18 mer
.18486
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.18495
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.18498
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                                                         8 copies 20 .18546
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                repeat: matches 286. .387
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                                                                                                                                                                                                                              ccacgaggccagcacccagggtcggacctgtgagccagagcatagcaagggtgggggcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                        gctggtgcggcgggagctgccgggggtgcggcagagtgccctggactacttcatgttcgc 812
                                          agagagcaagaagaggaagctggagctgagccggcggggagcagccgccacagggccagg
                                                                                                  GAGCCAGGGGGATGAGGCAGGGGGGCCACGGGGAAGATAGGCCGGAGCCCTTAAGCCCCAA
                                                                                                                 gagccagggggatgaggcagggggccacgggggaagataggccgggagcccttaagcccccaa
                                                                                                                                                         GGTGGACGAGGGGCCCCAGCCACGGAGCGTGGAGCCCCAGGATGCGGGACCCCTGGAGAG
                                                                                                                                                                      ggtggacgaggggccccagcccacggagcgtggagccccaggatgcgggacccctggagag
                                                                                                                                                                                                               CCACGAGGCCAGCACCCAGGGTCGGACCTGTGGGCCAGAGCATAGCAAGGGTGGGGGCAG
                                                                                                                                                                                                                                                                      CCGCTGCAAGTTCGTCTGGGGGCCCCCAAGACAAGCTGCGGAGGTTCAAGCCCAGCTCTCT
                                                                                                                                                                                                                                                                                                                                           ccgctgcaagttcgtctgggggccccaagacaagctgcggaggttcaagcccagctctct
                                                                                                                                                                                                                                                                                                                                                                                      CGTGCGCTGCCGACACCAGCGCCGCCAGCTGGTGCACTTCGCCTGGGAGCACTTCCGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="4 copies 34 mer 88% c
19457. 19604
/note="2 copies 74 mer 81% c
19546. 19625
/note="4 copies 20 mer 76% c
19839. 19954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="2 copies 51 mer 90% conserved" 20722. .20806 // note="5 copies 17 mer 89% conserved" 21349. .21410 // note="2 copies 31 mer 93% conserved" 21584. .21654 // note="LTR164 repeat: matches 88. .158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Alu repeat: matches 238. .311 24787. .24847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="MLT1D repeat: matches 107.
25853. .26065
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24855. .25064
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/note="2 cops
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Direct Submission
Submitted (10-DEC-1998) Cell Biology, Univ.
Birmingham, VH 302, Room 605, Birmingham,
Location/Qualifiers
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AF172450.1 G
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Regon, I.S., Verderame, M.F., Allen, S.S. and McLaughlin, P.J.

Cloning, sequencing, chromosomal location, and function of encoding an opioid growth factor receptor (OGFr) in humans Brain Res. 856 (1-2), 75-83 (2000)
                                                                                                                                                                                                           Direct Submission Submitted (26-JUL-1999) Department
                                                                                                                                                                    Pennsylvania State University
Drive, Hershey, pA 17033, USA
Location/Qualifiers
                                                                                                                                                                                                                                      Zagon, I.S., Verderame, M.F.,
                                                                                                                                                                                                                                                                                                                                              Eukaryota;
Mammalia; 1
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                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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alternatively spliced"
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Zagon,I.S., Verderame,M.F., Allen,S.S. and
Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; F
1 (bases 1 to 1232)
2 agon, I.S. Verderame, M.F., Allen, S.S. and
Cloning, sequencing, chromosomal location,
encoding an opioid growth factor receptor (
Brain Res. 856 (1-2), 75-83 (2000)
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gcgccactggtccgcttcttcctggaggagacgctggtgcggcgggagctgccgcggggggtt
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                                                                                                                                               TACATCCAGTGGCTGTTTCCTCTGCGAGAACCAGGAGTGAACTGGCATGCCAAGCCCCTC
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alternatively spliced"
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Pred. No. 4.7e-135;
D; Mismatches 5;
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Mammalia; F
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Submitted (04-JUN-1999) Neuroscience and Anatomy, Penn State University College of Medicine, 500 University Drive, Hershey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zagon, I.S., Verderame, M.F., Allen, S.S. and McLaughlin, P.J. Cloning, sequencing, expression and function of a cDNA encreceptor for the opioid growth factor, [Met(5)]enkephalin Brain Res. 849 (1-2), 147-154 (1999)
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; Eutheria;
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GGGACCAGGGCAGATAAAGATGAGGGCTCCAGGGACCCCTCCCAAGAGGCTTGGCAC
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                                                                                                                                                                                            AGAACACTACCAGGCACCCCTGGTCCGCTTCTTCCTGGAGGAGACCCTTGTACAGCACAA
                                                                                                                                                                                                        cgagcacttccaggcgccactggtccgcttcttcctggaggagacgctggtgcggggga
                                                                                                                                                                                                                                                                          GGCACGGGTGCTGTATGCCGTGCACAGAACTTCCAGCCGCGCTTCCACAATCTGAACAG
                                                                                                                                                                                                                                                                                       aggcacgggcacggtgggccgagcacagaactaccagaagcgcttccagaacctgaactg
                                                                                                                                                                                                                                                                                                                  GCGTCTTGTCCGGGCCTATGAGCTCATGCTGGGCTTCTATGGGTTCCACCTTGAGGACCG
                                                                                                                                                                                                                                                                                                                               9c9gcttgtccgggcctacgagctcatgctgggcttctacgggatccggctggaggaccg
                                                                                                                                                                                                                                                                                                                                                                    tgccaagccctcacgctcagggaggtcgaggtgtttaaaagctcccaggagatccagga
                                                                                                                                                                                                                                                                                                                                                                                               CGCCAAGCCCCTCACCCTGAAGGAGGTTGAGGCATTTAAAAGCTCCAAGGAAGTCAGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  agactgcaatggggacacgccaaacctgagtttctacagaaatgagatccgcttcctgcc
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JOURNAL
MEDLINE
REFERENCE
AUTHORS
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AUTHORS
TITLE
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SOURCE
ORGANISM
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HHU92288/c
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1 (bases 1 to 30752)

Kosuge, H., Isegawa, Y. and Yamanishi, K.

Nucleotide sequence analysis of a 30-kilobase-pair herpesvirus-6B (HHV-6B) genome and strain-specific virus Res 52 (1), 1-14 (1997)

98115230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGGAAGTTGGAGGGAACAGGCAGGAGCAGGTCCCAGGGGAGGCAGATCCCCAGGGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 30752)

Rosuge,H., Isegawa,Y. and Yamanishi,K.

Direct Submission
Submitted (07-MAR-1997) Virology, Research Institute
Diseases, Osaka University, 3-1 Yamada-oka, Suita, Os
Location,Qualifiers
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herpesvirus
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                                                                                                                                                                                                                                                                                                                                                                                               organism="Human herpesvirus"
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                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                        LHTVVFFYWFYNALYKTPLYENGIVPCIVCVGSPTQSNALVTSENPLTQNKDVRGID
VLSALLCDDVLSKYCEVDNNWIIFVNNKRCADHAFGDFLKHEEFGLPLKPELLEYVDQ
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TFEDYKSEIGNESLEIPPWFKSNIHRLMTYSOFADQDLSKTVOLEEIYLEDGSVEETL
ITCHLKHIRNSSIGVTSKIKASTVGFSGTYEKFVELLQSDLFIEKTSCEQTIHAYSFL
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GLVDDGLSDMDLLEIDPGGDFFTRYSKIPFLNSLSFEEISLLYTTFKDIFISRFAIL
QMHTKGXFKYLLVTYKRNNVSRKQCGEIYSHLKSFYGMLTVAIPANNFLEGYTNDN
VVHLGTDKQLPQILYKKGLPRLVIKDEMGFISVLDNNVSKFVDVVNGQSFHLCTTVDY
ATVSKYSMTITKSQGLSIQKVAILDFGSDPKNLKLSSIYVGMSRVTDPNNLIMNVNPLR
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/gene="H76"
complement(1974. .3962)
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/note="similar to HHV6A U76, HCMV UL104, HVS gene 43,
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ILGAEISNIINFILQSINNSHYNRYUDWICTVGIVPFWRTTPTAPNLYNLLQQVSSKLI
HDIVRHKQNIVTPILLGLSSVIIPDFHNIKIFRDRNSEQISGFKNKKAIAFFTYSTPY
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ERSIQIQQKQDLSIYWNVISDIAERALGAVACKTKELPDLCE$SVIVIDEAGVILRHI
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NIFSPNPENEILEKIKRIRNLRRIQHLTRPNYPKGDQD"
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9838. 10449
9838. 10449
9838. 10449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="CB6RH"
8179. .8406
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8829. 9866
8829. 9866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(10493. .11260)
/gene="H81"
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DMRVFETETTQNARRVRQRTRTTVGSTDGAIGQQRVISGQNRGRARGRGRGRVPRRRN
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complement(11336. .12088)
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VNFFIIGVSRSWTFLNSICFVVISEPPKEKRQKSHHETKRNLEEQSHEDGIAPTSTTF
VNGAVEGALSPCVSIDNHEDQQHDELDKRVYAQVGGVLGSPKPRSLESLLCVSKADLF
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SGTCETFSKGWISMIYWTSETDSMGSLTVDIGMDEGKCRTYRARGLLLCSKSITSISQ
NTEGRERILTVSHENGKLQITFVTIAKVSSEPELRNLGDLKFWEKFEKECRALDRKKH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(11336.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to HHV6A U81,
3KRF3, EHV1 61, VZV 59, HSV1
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Submitted (18-DEC-1998) to the DDBJ/EMBL/GenBank databases. Yuji
Isegawa, Osaka University Medical School, Department of
                                                                                     J. Virol. 73 (10),
99412319
                                                                                                                          Isegawa,Y., Mukai,T., Nakano,K., Kagawa,M., Chen,J., Mori,Y., Sunagawa,T., Kawanishi,K., Sashihara,J., Hata,A., Zou,P., Kosand Yamanishi,K.
COmparison of the complete DNA sequences of human herpesvirus
                                                                                                                                                                                                                                                                                                                 Human
                                                          Isegawa, Y
                                                                                                                variants A and B
                                                                                                                                                                                                        Human herpesvirus 6 (strain:HST, pop_variant:B) DNA. Human herpesvirus 6 Viruses; no RNA stage; Herpesviridae;
                                                                                                                                                                    Isegawa, Y., Mukai, T.,
                                                                                                                                                                                                 Betaherpesvirinae; Roseolovirus.
                                                                                                                                                                                                                                                                          AB021506.1
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llarity 55.0%;
Conservative
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12057. .12506
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12057. .12506
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                                                                                                                       DNA sequences of human herpesvirus
                                                                                                                                                                                                                                                                                                              variant:B,
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.6e-12;
                                                                                                                                                                                                                                                                                                            strain:HST, virion
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                                                                               /gene="DR2"
1027. .2970
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/note="68.2%
                                            complement (5023.
                                                                       complement(5023.
                                                                                                                                                                                                                                complement(2718. .3320)
/gene="DR3"
/note="ORF unique
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                'note="ORF
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                                                           /gene="DRHN1"
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VPSSASPSAPCIGRSRPPSAQTA"
                                                                                                                                                                         /codon_start=
                                                                                                                                                                                  /note="82.5% identical to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US22 gene family"
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/translation="MPLPARVSHALHRLPLSHYWWLLLGRHSLRHVHSYLRLHKGLRL
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576. .842
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/gene="LT1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="LT1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="DR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="86.4% identical to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10368"
/pop_variant="B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="52.5% identical to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="HST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ∕organism="Human herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
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              HST strain"
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                           HHV-6"
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                                                                                                                                                                                                                                                                             /gene="DRHN2"
complement(7236. .7706)
gene="DRHN2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLWPDARRQLRLHLYAGHPLGPWIVCAVLSRERETQTPSPPIGSGGVTLGNVPTPGPR EVETAWVIVTWRDRCYRSGPITARSAVWRTRSPPCGGWAAGHERTLDVFGPG" complement(7236. .7706)
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6512. .
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                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene-"DR8"
7928. .8662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mlappiprgvyIkgecgalssspdlcDspcrvgigrcysnsarg
RRCLTDRKYVFflLCGvSnterkHIvCDCvHspilfliglkagrdtvtrtythpthtr
RRIDISTAVLLflflrtphffffvLyfeilvMiflrsCLwpyIaslrlrrgv"
                                                                                                                                                                                                                               complement(8292.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="transactivator"
/protein_id="BAA78217.1"
/db_xref="GI:4995984"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9-AHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="DR7"
/gene="DR7"
/function="transforming activity"
/note="42.2% identical to DR7 gene of strain Ull02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="BAA78216.1"
/db_xref="GI:4995983"
/translation="MTTHYOMROGRIAIRRDGARLAHARARARFEWLLLARGRPSKL
YGYTSRHRGERIHLPWPRYWCLELHPDPYRDARSATVWGHRWGWPPTHVRPRSVQDCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "9-VHH
                                                                                                                                                       /gene="LJ1"
/note="16.6% identical toLJ1 gene
                                                                                                                                                                                                          /gene="LJ1"
                                                                                                                                                                                                                                                                                                                                                                                                      /gene="DR8"
/note="13.6% identical to DR8 gene of strain Ull02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="BAA78218.1"
/db_xref="GI:4995985"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="DR6"
/note="84.5% identical to DR6 gene of strain Ull02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="DR6"
5025. .5336
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/db_xref="GI:4995982"
                                                                                                                         /codon_start=1
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                "GLGTGTGT"
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Best Local Similarity
Matches 273; Conserv
129013 GCAGAGCCTCCAGCAGAGCC 128994
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                                                                                                                                                         GCAGGGCCTCCAGCAGAGCTTCCAGCAGAGCCTCCAGCAGGGCCTCCAGCAGAGCCTCCA
                                                                                                                                                                                GAAGAGCCTCCAGCAGGGCCTCCAGCAGAGCCTCCAGCAGAGCCTCCCA
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                                     agggatgagccagccaaggc
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8929 .9384
/gene="U1"
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/db_xref="GI:4995989"
/tdb_xref="GI:4995989"
/translation="MCSQFCGRSVHFHFRGRRREYDSTLFVSNSCSYLNVIVDVYVR
/translation="MCSQFCGRSVHFHFRGRRREYDSTLFVSNSCSYLNVIVDVYVR
LPVTLPLSFFFFFILLILSRIPHRKKMFCRSPFEIGISSWSLASAALCPSSCSFSAGRD
LRCDAAVPEVKWTAFVRTLVARPLSADDVRDFVSTFAHCRLALSWPVGAELRFATSDM
RLGITQAELAKLSRGYGCCFGMDLTVIGVTIFAEVSALVLVGECGEIYAFNGVEDDALY
RLGITQAELAKLSRGYGCCFGYGVTVLFTGASFFGRGVTLDLLAFAVSFALVPLP
WPRGAEFFEFAUFRREKRWILIFGGGVAVVIGRFFGRGVTLPLLRRQRVLMDQVGRVY
AASLDGGAVVRLSDSFRAFLAMGVRKLFKNHRRPPGHLMTMQLPVTCVHAPVINLPAV
YQLSPHMVEREMSAVSCGASTYVRRDCEDTLRDGDAGVDTS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(9467. .10768)
/gene="U2"
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/gene="U2"
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/db_xref="GI:4995988"
/translation="maraperraidlstdprpisvmqirtrtrtdmptrphradchvse
/translation="maraperraidlstdprpisvmqirtrtrtdmptrphradchvse
sinthekihtekytqenthtokythkkihtokkihthkkihtoknthtoknt
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/gene="U3"
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Pred. No. 3.8e-12;
0; Mismatches 227;
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J. Virol. 73 (10), 8040-8052 (1999)

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7 (here-
                9 (bases 1 to 162114)
Pellett, P.E., Dominguez, G., Dambaugh, T.R.,
and Inoue, N.
                                                     GA 30333, USA
9 (bases 1 to
                                                                                        Direct Submission Submitted (02-OCT-1993) Control and Prevention,
                                                                                                                                                                        Control and Prevention,
GA 30333, USA
8 (bases 64106 to 8496
                                                                                                                                                                                                   Submitted (26-\overline{J}0L-1993) Herpesvirus Section, Centers for Disease Control and Prevention, 1600 Clifton Road, Mailstop G18, Atlanta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lindquester,G.J., Greenamoyer,C.A., Anton,E.D., O'Brian,J.J., Pellett,P.E. and Dambaugh,T.R.
Comparison of a 20 kb region of human herpesvirus 6B with other human beta herpesviruses reveals conserved replication genes and adjacent divergent open reading frames
Arch. Virol. 142 (1), 193-204 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lindquester,G.J., O'Brian,J.J., Anton,E.D., Greenamoyer,C.A., Pellett,P.E. and Dambaugh,T.R.
Genetic content of a 20.9 kb segment of human herpesvirus 6B strain 229 spanning the homologs of human herpesvirus 6A genes U40-57 and containing the origin of DNA replication
Arch. Virol. 142 (1), 103-123 (1997)
                                                                                                                                                   Pellett, P.E.
                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                    Pellett, P.E
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1 (bases 19696 to 22886)

Pellett, P.E., Sanchez-Martinez, D., Dominguez, G., Black, J.B., Anton, E., Greenamoyer, C. and Dambaugh, T.R.

A strongly immunoreactive virion protein of human herpesvirus 6 variant B strain 239: identification and characterization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Restriction endonuclease mapping and molecular cloning of the human herpesvirus 6 variant B strain 229 genome Arch. Virol. 141 (2), 367-379 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 (bases 64106 to 84963; 106012 to 126166)
Lindquester,G.J., Inoue,N., Allen,R.D., Castelli,J.W.,
Dambaugh,T.R., O'Brian,J.J., Danovich,R.M., Frenkel,N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Intragenomic linear amplification of human herpesvirus 6B oriLyt suggests acquisition of oriLyt by transposition J. Virol. 69 (1), 589-596 (1995)
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Stanmey, F.R., Dominguez, G., Black, J.B., Dambaugh, T.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene and mapping of a variant-specific monoclonal antibody reactive
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Human herpesvirus 6B
Viruses; dsDNA viruses,
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Human herpesvirus 6B strain Z29, complete genome.
AF157706 L13162 L14772 L16947
AF157706.1 GI:5733510
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                                                                                        Herpesvirus 9
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n Road, Mailstop (
                          Stamey, F.R., Dewhurst,
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GA 30333, USA
Sequence updated by submitter
on Aug 16, 1999 this sequence
g1:305397.
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Submitted (10-JUN-1999) Herpesvirus Section,
Control and Prevention, 1600 Clifton Road, M
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join(583. .841,95
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/strain="Z29"
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Ygytsrhrgerillpprywclelhpdpyrdarsatywgghrwewpthyrprsyydca
LDSSLYVCCGYGEKLOPVGFYSSYLTHSPLDTLRVLLVGROGAVYVHHRABARLCTLA
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VCAVLSRERETQTPS$P 1GSGGVILGNVPTPGPREVETAWYIVTVAGFLLSTWPDIGK
VCAVLSRERETQTPS$P 1GSGGVILGNVPTPGPREVETAWYIVTVAGFLLSTWPDIGK
CRLANSFAALMRMGPRAMRGHWTYSAPGRHLPGDAWPLCEHVRPPVGKLPRQRAYLD
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3938. .3942
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D; Mismatches 228;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soergel, A., Schiewe, U., Fleckenstein, B. and Neipel, F. Identification of an human herpesvirus-6 transcription unit homologous to the immediate-early 2 gene of human cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human herpesvirus 6 (strain Uganda-1102).
Human herpesvirus 6 (strain Uganda-1102)
Viruses; dsDNA viruses, no RNA stage; Her
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human herpesvirus
AF015297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soergel, A., Schiewe, U., Direct Submission
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1 (bases 1 to 4742)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                evidence for early/late
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/product="IE2hom"
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SNESCSTQVRRASELPMQLAPMYTSHRQNANLQNNTTSLPVQPYRDYRDIESSYRE
SRNTNRGYDYNFRHPYRPRGGNGKINYYNPNSKYQQPYRCFTRTYNRRGRGHRSYD
CSDRSADLPYSHYTYPMYEQQNPDPRMNNYKDFTQLTNKFFESTDYSMAFSTDSTHY
QSDNYNHPTRAQTIEDTTKTKKHEATKONETSTENGVLTPDVISLYSTPSSYKMDIIK
KIYDTDVIPLPKEALTANGSNADVDIQXYKKAHIRCRSVQKKERSSQTNKHDENHAS
SRSDLKERKSNENENGAVTKARDFSKLNPLLSPLPLTPEBAIDPADHTDKFYSTEREN
SRSDLKERKSNENENGAVTKARDFSKLNPLLSPLPLTPEBAIDPADHTDKFYSTEREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D-91054, Germany
                                                                                                                                                                                                                                                                       cytomegalovirus"
                                                                                                                                                                                                                                                                                                                                       196. .4698
                                                                                                                                                                                                                                                                                          /note="similar to
                                                                                                                                                                                                                                                                                                                  /gene="ie2hom"
                                                                                                                                                                                                                                                                                                                                                         /gene="ie2hom"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                 organism="Human herpesvirus"
db_xref="taxon:10370"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                             the immediate-early 2 protein of human
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                                                                                                                                                                                                                                                                                                                                    GGGATTCTAGCAGGGCCTCAAGCAAAGCCTCCAGCAGAGCCTCCAGCAGGGGATTCTAGCA 2779
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Human herpesvirus 6.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Roseolovirus.
1 (bases 1 to 13965)
Soergel,A., Schiewe,U., Fleckenstein,B. and Neipel,F.
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FEYKQIPKKPCNEKNLKEAVYDICCNGLSNNAAIIMYFTRSKKVAQIIKIMQKELMIR
PNITVSEAFKMNHAPPKYYDKDEIKRFIQLQKQGPQELWDKFENNTTHDLFSRHSDVK
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VERSION KEYWORDS

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Matches 256
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GAGCCTCCAGCAGAGCCTCCAGCAGAGCCTCCAGCAGGGATTCTAGCAGGGCCTCAAGCA 10018
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Direct Submission
Submitted (21-JUL-1997) Institut fu
Virologie, Universitaet Erlangen Ni
Erlangen D-91054, Germany
Location/Qualifiers
                                               gagageceateggagaececeaggeececegeeaggaectgeaggggaegageeagee 1818
                                                                           GGGATTCTAGCAGAGCCTCCAGTAGAGCCTCCAGCAGGGCCTCAAGCAAAGCCTCCAGCA
                                                                                         gagageceateggagaececaggeeceggeeggaeggaeetgeaggggaegageeagee 1758
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TMIIYAATPIDFYGAYKTCNKYAKDNPKEIYLRYCSIIDGDNPISIYNPISKEFKSKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="IE-2 protein"
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/db_xref="GI:2384715"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(1846. .1904,1993. .2186,7868. .12117)
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/db_xref="taxon:10368"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="ie2hom"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Human herpesvirus
                                                                                                                                                                                                                        53.4%;
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Pred. No. 1.5e-09;
0; Mismatches 22:
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AUTHORS
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Human herpesvirus 6 replication origin-binding protein (HDRFO), partial cds, helicase-primase component (HDRF1), virion protein (HDLF1), putative helicase (HDRF2), putative phosphoprotein (EDRF1), replication protein (EDRF2), putative uracil-DNA glycosylase (EDLF4), putative gL glycoprotein (EDLF3), putative gL glycoprotein (EDLF3), putative glycoprotein (EDLF3) genes, complete cds, and major immediate-early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        용
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequence analysis of a 21-kbp region of the genome of human herpesvirus-6 containing homologues of human cytomegalovirumajor immediate-early and replication genes

Virology 204 (2), 738-750 (1994)
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1 (bases 1 to 21191)
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Human herpesvirus 6
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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U13194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U13194.1 GI:862477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21231, USA
Jun 17, 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 21191)
CDEYFVLGDISGVYEWGMLIDLAFLAEMIRKDLKLKSCTDTTTDISEDDLLLCAARRS
SDILQIMQLVFTVHVQFFQKYSLQTLQLFNKLRGMRIVTGVFSIEKFSISILRLFFKC
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/db_xref="GI:662096"
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/db_xref="taxon:10368"
/clone="HindIII-D, EcoRI-D, p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Human herpesvirus"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="HDRF0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /map="109-130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="U1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1995 this sequence version replaced gi:662095
                                                                                                                                                                                                                                                                                                                                                                                                                   .1980
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/evidence=not_exp
complement(3939.
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VIRNKLMLTTPLAHLSPELKKHNSLRRHQKMCQLLNTFPIKVLTTAKTDYTNKKIMDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MKSLKKLKELETSDVFNILHVRTILKVIKIDKCISLARHPLVNI
TVGDDGIWFHLEDGTMINGLEKKTICERELGFOGFIGIIILDSEDTLQELKLUPFQFK
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TLVCTLRHIFFNEHASEILHKVPLMIRLYNEMKNTHIEVLELYFNTKRSHNFINLSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene-"HDRFO"
3790. .3795
                     IEKBEKSSDAKKSLI KFLLMLSDSKKKIG INDSVEGFI PEITPSI IDONKLMLNRGOF
RKRSA IDTGERDVRDLFKKQ II KCMEEQ IQT DET IKTTNOMFERK IKDLHSLLE
TNNDCDRYMPNLDHDLENLSLSRALMI VQRLPFTSVSI DDTRGVANSFFSQY I PDTQ
ADKRI DQLMEMEYMRT FRLRKNVNNQGQEES I TYSNYSI ELL IVPFLRRFLNI YNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(4630. .6618)
/gene="HDLF1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar
Number L14772"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence=not_experimental complement(3939. .6618) /gene="HDLF1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKKIRFGYSVMDFHFSLTVSDVKICFSHTDTGEAVCEKMKQIFSFSVCAFGGGQVLLV
TPKNRXALLFDDDLCLLLLQSVFAFLHEKIFGYVKOLVDYLCEYIGPDLMPFGNERSV
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PGSETSLQRFRFNSQYVSSESLCFQTGPEDTHLFFSDSDMYVVTLPDCLRLLLKSTVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MHLRGCACHLSLYCVYNDWENKIYRVPIFQCLFLEAETRSLKTF
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FVPLTVVLGDDGLEILEAYVCGEELMLPLDTVPVILRCIGDYAALDTKHLLSNECTQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental 3790. .3795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRVLRRWVESKFEDVEQTQFIRWENRMLCEHIHLLHLN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RFFLSSGLSQSKEAHWTVTASKYLSACIRTNKTGLCFASITVYFQDMMCVFIANRYNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAFLPCFDENATEIDLLLKFMSRLQHRSYALFDAVIFMLDAFVSAFQRACTLMGMRWL
LVRDLHMFYLTCDGKDTHVVMPLLQTAVENCWEKTTEIKQRPTFQCAEISRCGFIVYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="unknown"
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/db_xref="GI:662097"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="component of helicase-primase complex; similar to HCMY UL102 Swiss-Prot Accession Number P16827"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAA68466.1"
/db_xref="GI:662098"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                              'note="similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene-"HDRF1"
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39. .4721)
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Query Match
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LHTVVFFYWFYNALYKTPLYEDGIVPCIVCVGSPTQSNALVTSFNPLTQNKDYKRGID
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FVKPASYIRNEMMEIETTRLFLSHNEVKNYFRSLHEQVEVTNRNNLFVFPVYFLIKNK
IFEDYKSEIGNFSLEIETWFKSNIHRLNTYSQFADQDLSKTVQLEEIVLEDGSVEFTL
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VYHLGTDKQLEQILYKNGLPRLVIKDEMGFSTSHLKSFYGMLTYALTANNYTLEGYVNDY
ATVERCENT THE GETTE STLLYTN THE GETTSTATTET TOTT THE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="replication"
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Swiss-Prot Accession Number P17151"
                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="EDRF2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="putative phosphoprotein; similar to HH6 CB7R, GenBank Accession Number L14772 and HCMV UL112, Swiss-Prot Accession Number P16768"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDEPRRSIQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAA68470.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental complement(10022. .10351)
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                                                                                                                                                                                                                                                                                                                 codon_start=]
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11477. .12511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="EDRF1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'product="unknown"
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/gene="HDRF2"
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                                              19136 AAGCCTCAAGAAAAGCCTCCAGCAGAGCCTCCAGCAGGGCTTCCAGCAGGGCCTCAAGCA 19077
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                   1999 gagagcccatcggagaccccaggccccagcccggcaggacctaca 2043
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Search completed: October 12, 2000, 17:56:51 Job time: 34787 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

c 111	. 4 10 10 12 80 02		Result
105.4 103.2 101.4	2118.6 1555.6 1542.8 1351 977.4	2276.4	Score
	592.5 67.9 59.0 42.7	99.4	% Query Match
161573 162114	2423 160241 6670 1676 1232 2208	2363	Length DB
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GPKEGTPGSPSETPGFSPAGPADDEPAESPSETFGFRAGAGSPSETFGFSP
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Zagon, I.S., Verderame, M.F., Allen, S.S. and McLaughlin, P.J. Cloning, Sequencing, Chromosomal location, and function of encoding an optoid growth factor receptor (OGFr) in humans primares. 856 (1-2), 75-83 (2000)
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Submitted (26-JUL-1999) Department of
Pennsylvania State University College
Drive, Hershey, PA 17033, USA
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Zagon, I.S., Verderame, M.F., Allen, S.S. and McLaughlin, P.J. Cloning; Sequencing, chromosomal location, and function of encoding an opioid growth factor receptor (OGFr) in humans Brain Res. 856 (1-2), 75-83 (2000)
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                                                                                                                                                                                                              Liu, J., Brewton, R.G., Takanosu, M., Direct Submission
                                                                                                                                                                                                                                                 Unpublished
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FRAPCKEYWGPQDKLRREKPSSLPHPLEGSRKVEEEGGPGDDPLEASTQGRMCGPEHS
KGGGRVDEGPQRRSVEPQDAGPLERSQGDEAGGHGEDRPEPLSPKESKKKRKLEBRE
QPPTEPGPQSASEVEKIALNLEGCALSQGSLRMGTGTQEWGGDDGEAVQPCRQPLGARV
ADKVRKRKVDEGAGDSAAVASGGAQTLALAGSPAPSGHPKAGHSENGVEEDTEGRTG
RKGTPGSPSETPGPSPAGPAGDEPAESPSETPGPRPAGPAGDEPAESPSETPGPPRPA
GPAGDEPAKTPSETPGPSPAGFTGDEPAKSPSETPGPRPAGPAGDEPAESPSETPGPRPA
GPAGDEPAKTPSETPGPSPAGFTRDEPAKAGEAAELQDAEVESSAKSGKP"
PAGPAGDEPAESPSETPGTSPAGFTRDEPAKAGEAAELQDAEVESSAKSGKP
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Em: EMBL: Sw. SWISSPROT; Tr. TREMBL: Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr20 RP5-85L7 is from the library RPCI-5 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                          This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                              Submitted (09-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 8, 2000 this sequence version replaced gi:8919619.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                         This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Human DNA sequence from
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     equence is the entire insert of clone RP5-885L7 clone RP4-563E14 is at 140192 in this sequence
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                /note="13 copies 4 mer 14394. .14478
                                                                                   /note="AluY repeat: 10876. .10962
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note="11 comiss of mer 77% conserved"
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single clone. Assembly consistent with restriction
                                                                 'note="MIR repeat: matches 86.
                                                                                                                                  /note="MER68A repeat: matches 68. .210 of consensus"
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354. .397
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/clone="RP5-885L7"
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/db_xref="taxon:9606"
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.5163
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/note="15 copies 19 mer from 16593..16872

/note="17 con".
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20722. 20806
/note="5 cor"
21349.
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19546. 19625
/note="4 cor;
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18497. .18546
/note="25 copies 2 mer ac 72% c
19329. .19433
/note="LTR16C repeat: matches 20
19455. .19590
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/note="8 copies
18407
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20704. .20805
/note-"3 copies 34 m
20710. .20811
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18320 .18495
/note="44 copies 4 mer a
18321 .18496
/note="11 copies 16 mer
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/note="4 copies 48 n
18317. .18496
/note="3 copies 60 n
18319. .18486
/note="7 copies 24 m
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16644. 116885
/note="3 copies 74 mer 7
16670. 116904
/note="5 copies 47 mer 7
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/note="5 copies 48 | 16603. .16842

/note="3 copies 80 | 16638. .16901
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/note="10 copies 31 m
16583. .16879
/note="9 copies 33 me
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16848. .16999
/note="13 copies 4 mer gaag 100% conserved"
17287. .17411
/note="MEE5A repeat: matches 35. .165 of consensus"
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/note="17 copies 4 mer tccc
16266. .16577
/note="Alusg repeat: matches
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/note="5 copies 40
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/note="11 copies 24
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/note="17 copies 17
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21584. 21594
/note="LTRAIGA repeat: matches 88. .15
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Direct Submission
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2 Tagon, I.S., Verderame, M.F., Allen, S. S. and McLaughlin, P.J. Cloning, sequencing, chromosomal location, and function of encoding an opioid growth factor receptor (OGFr) in humans paragraphs. 856 (1-2), 75-83 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pennsylvania State University Drive, Hershey, PA 17033, USA Location/Qualifiers
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Direct Submission
Submitted (26-JUL-1999) Department
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/db_xref="gr: 7595301"
/db_xref="gr: 7595301"
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QEIQERLVRAFELHGGYGIRLEDNHSTGTVGKAQNYQKREQNLAWRSHNNLRITRILK
SPCELSLEHFOADLVREFLEETILVRRELPGVRQSALDYEMFAVRCRHQRROLVHFAWE
HFRPRCKFVWGPQDKLRRFKPSSLPHPLEGSRKVEEGSSPGDPDHEASTQGRTCGPEH
SKGGGRVDEGFQPRSVEFQDAGFLERSGGDEAGGHGEDRPEPLSPKESKKKKLELSRR
EQPPTEPGPQSASEVEKIALNLEGCALSQGSLRTGTQEVGGQDDFGEASCPCCRGWGLR
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alternatively spliced"
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/db_xref="taxon:9606"
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Zagon, I.S., Verderame, M.F., Allen, S.S. and McLaughlin, P.J. Cloning, sequencing, chromosomal location, and function of encoding an opioid growth factor receptor (OGFr) in humans Brain Res. 856 (1-2), 75-83 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (26-JUL-1999) Department of Neuroscience and Pennsylvania State University College of Medicine, 500 Drive, Hershey, Pa 17033, USA Location/Qualifiers
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Zagon, I.S., Verderame, M.F., Allen, S.S.
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/map="20q13.3"
/clone="127"
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SPCELSLEHFQAPLVREFYEILFTLEFTLYRRILFGVRQSALDYFMFAVRCRHGRRQLVHFAWE
HTRPRCKFYWGPQDKLRFFKPSSLPHPLEGSRKVEEEGFAGDEPAESPSETFGFPSPAG
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alternatively spliced"
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/db_xref="GI:7595299"
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Mammalia; Eutheria; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
ORGANISM
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HHU92288/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCTGAGGGTGATGGAGTAGT-----CAGTAACACTCAAATGCAGGCCAGTGCCCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T-----
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U92288
U92288.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 30752)
Kosuge, H., Isegawa, Y. and Yamanishi, K.
Direct Submission
Submitted (07-MAR-1997) Virology, Rese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 30752)

Rosuge, H., Isegawa, Y. and Yamanishi, K.

Nuclectide sequence analysis of a 30-kilobase-pair
herpesvirus-6B (HHV-6B) genome and strain-specific
major immediate-early genes

Virus Res. 52 (1), 1-14 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human herpesvirus 6
Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vriuses; asunA viruses, no RNA (
Betaherpesvirinae; Roseolovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human
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Human herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L5230
                                                                                                                                                                                                       /codon_start=1
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TSLORFRENSQYVSSESLCFQTepEDFHLFFSDSDMYVYTLPOLTALLKSTYPKAFL
PCFDENATEIELLLKENSPALGHRSYALFDAVIFMLDAFVSAFQRACTLMEMRWLLVRD
LHVFYLTCDGKDSHVVMFLLQTAVENCWEKITELKGRPAFQCMEISRGGFVFYARFFL
SSGLSQSKEAHWFYTASKYLSAAIRANKTGLCFASITVYFQDM%CVFIANRYNVSYWI
EEFDPNDYCLEYHEGLLDCSRYTAVMSEDGQLVRQARGIALTDKINFSYYILVTLRVL
RRWYESKFEDYSGTEFIEWENRALYEHIHLLHLN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            herpesvirus
                                  /note="similar to HHV6A U:
BBRF2, EHV1 55, VZV 53, H2
/codon_start=1
/product="H75"
/protein_id="AAC40325.1"
/db_xref="GI:2769713"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene-"H75"
                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="H74"
/function="replication, helicase-primase complex"
/note-"part of helicase-primase complex, similar to
/note-"part of helicase-primase complex, similar to
U74, HCMV UL102, HVS gene 41, EBV BBLF3, EHV1 54, VZ
HSV1 UL8"
/translation="MKSLKKLKELETSDVFNTLHVRTILKVIKIDKCVSLARHSLVNI
TVGDDGIWFHLEDGTMINGLEYKTICEKELGFQGFIGIIILDSEDTLQELRLNPFQFK
                                                                                                                                                                          /gene="H75"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="H74"
<1. .1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /serotype="B"
/isolate="HST"
/db_xref="taxon:10368"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (07-MAR-1997) Virology, Research Osaka University, 3-1 Yamada-oka, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism-"Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:2769711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g g
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                                                                                                       to HHV6A U75,
, VZV 53, HSV1
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                                                                                                                                                                                          . 2065)
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                                                                                                       HCMV
UL7"
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                                                                                                                       OL103,
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immediate-early
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Osaka
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565, Japar
                                                                                                                     42,
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VZV 52,
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gene
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/gene="H77"
/function="helicase, helicase-primase complex"
/note="similar to HHV6A U77, HCMV UIL105, HVS gene 44,
BBLF4, EHV1 57, VZV 55, HSV1 UL5"
/codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="#17"
/protein_id="Ac40327.1"
/protein_id="Ac40327.1"
/protein_id="Ac40327.1"
/db_xref="G1:2769715"
/db_xref="G1:2769715"
/translation="MSISSLFGGRYDNKFLLNMSSAPKIELIVDKVASLSERRLEGRL
/EDWFRHIMDPETEFNSEFADALCIGIDEFAQPLPFLPFRALLYTGTAGAGKTNSIQT
LAANLDCIVFATTSIAAQULSYVLNRSKSAQVKTIFKTEFGFNSSHVSNSERGSYIAND
ERSIQIQQKQDLSIYMNVISDIAERALGAVACKTKELPDLCESSVIVIDEAGVILRHI
LHTVVFFYMFYNALYKTPLYENGIVPCLYCVGSPTQSALVTSENDLTQNKDVKRGID
LTGTVFFYMFYNALYKTPLYENGIVPCLYCVGSPTQSALVTSENDLTQNKDVKRGID
                                                                                                                                                                                                                             /gene-"CB6RH"
8179. .8406
                                                                                                                                                                                                                                                                                     /translation="MTSAKTNESLPRSTRMYSGGNLKNAQFSLLSSRELVNSYFDVNS
GGGLDGVLSINRSSFIFCTTEVILGIGVRIR"
8179. .8406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGLAFGGMYSFCCSEFTFPEVLMEIKNIKMPSIEFLBSEMSRASRDVQTVETDERYDF
GLVDDGLSDMDLLEIDPCGDPFFTRYSKLPLTNSLSFEETSLLXTTFKDIFISRFAIL
OMHTKKKFGKFLLVTYNRNNYSRKQCGEIYSHLKSFYCMLTYALPANNYTLEGYTNDV
VVHLGTDKQLPQILYKKGLPRLVIKDEMGFISVLDNNVSKFVDVVNGQSFHLCTTVDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILGAEDMLSKNLLSYLPPNNEEIDMIYPSEQIMTFIEMLHGHKNFFKGQTIHNALRDS
AVLKKQIAYGYAQALLNSVSIQQIHDEMKRHYRSEPFHNKLSPEDVISVMAHAIKQV
ILGDISNIINFILQSIDNSHYNRYDMICTVGIVPFMRTTBTAPNLYNLLQQVSSKLI
HDIVBHKQNIYTPILLGLSVIIPDFHNIKIFRDRNSEQISCFKNKKAIAFFTYSTPY
VIRNRLMLTTPLAHLSPELKKHNSLRRHQKMCQLLNTFPIKVLTTAKTDVTNKKIMDM
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                       /product="CB6RH"
/protein_id="AAC40343.1"
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/db_xref="61:2769731"
/tanslation="MLHNVSKCIHSICIRVCIKLHVICSSRESIRCFAVYETYSLIPN
TSDGRQAFLYAFYGKVHALVADAIRKGFRFG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="CB5RH"
6495. .6722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATYSKYSMTITKSQGLSIQKYAIDFGSDPKNLKLSSIYYGMSRYTDPNNLIMNYNPLF
LNYENDNFIAPHIYKALKNENTMLIF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLSALICDDVILSKYCEVDNINJI IFVNIKRCADHAFGDFLKHIEFGLPLKPELIEYVDQ
FVKPASYIRNPMNEIETTRLEISHNEYKYFRSLEGOVEVTNIKNLFVEFVYFLIKNI
TFEDYKSEIGNFSLEIEPWFKSHIHRLNTYSOFADODLSKTVOLEEIYLEDGSVEETL
ITCHLKHIRNSSIGVTSKIKASTVGFSGTYEKFVELLQSDLFIEKTSCEQTIHAYSFL
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NIFSPNPENEILEKIKRIRNLRRIQHLTRPNYPKGDQD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RKRSAIDTGERDVRDLFKKQIIKCMEEQIQTQMDEIETLKTTNQMFERKIKDLHSLLE
TNNDCDRYNPDLDHDLENLSLSRALNIVQRLPFTSVSIDDTRSVANSFFSQYIPDTQY
ADKRIDQLWEMEYMRTFRLRKNVNNQGQEESITYSNYSIELLLIVPFLRRLLNIYNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="possible virion protein"
/note="similar to HHV6A U76, HCMV UL104, HVS
BBRF1, EHV1 56, VZV 54, HSV1 UL6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(1974. .3962)
/gene="H76"
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/gene="H76"
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KLVCTLRHIFFNEHASEILHKVPPMIRLYNEMKNTHIEVLELYFNTKRSHNFINLSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAC40326.1"
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/translation="MHRASANSILNSVSGSMMWRNQSSGRRPSKRLSDNEATLSTINS
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                                                                                                                                                                                                                                                                                                                                                                                                                               /product="CB5RH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="CB5RH"
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                                                                                                                                                                     codon_start=1
                                                                                                                                                                                               gene="CB6RH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
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ş
                                                     Query Match
Best Local Sim
Matches 206;
                                                                                                                                                                                                                             gene
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1572 tacccctgggagcccatcggagaccccaggccccagcccagcaggacctgcaggggacga 1631
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                                                                                  Similarity
                                                        Conservative
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/gene="H80"
9838. .10449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="H79"
8829. .9866
/gene="H79"
                                                                                                                                                                  12057. .12506
/gene="H83"
12057. .12506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(11336. .12088)

/gene="H82"
/function="gH-gL complex, infection, cell fusion"
/note="gL; similar to HHV6A U88; HCMV UL115, HVS gene 47,
EBV BKRF2, EHV1 62, VZV 60, HSV1 UL1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(10493. .11260)
/gene="H81"
complement(10493. .11260)
/gene="H81"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="mtureglsnednygnfqluksleqlrarlyassgevverslskl
KERLDYVKDNLIKNVLECADVTVPSKCLSKTKHIEQKKQIVFSDCVRSVPVCEIKPFI
DMRVFETETTQNARRVRQRTRTTVGSTDGAIGQQRVISGQNRGRARGRGRGRVPRRRN
SNLNIKLRTQNSALVIDDSSETENFENAGSFNEDLLATTILETL"
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'gene-"H80"

function "possible replication protein"

/functions "possible replication protein"

/note-"start-codon ggg; similar to HHV6A

spliced in vitro replication protein"
                                                                                                                                                                                                                                                                               /translation="MELLLFVMSLILLTSKRAMPLFDHNSFYERKLDDCIAAVINCTR
SEVPLLLEPIYQAPVNEDVKSILLKPPTKKRPFSRIMVTNEFLSDFLLLQDNPEQLR
TLFALIGDDESRDMWLNFFMCFQTCSBSVGTTCISDNCRKYLPERITYVNNFFYDNI
AGLEFNISENTDSFYSNIGFLLYLENPATGITKIIRFPFNSLTLFDTILNCLKYFHLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(11336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to HHV6A U81,
BKRF3, EHV1 61, VZV 59, HSV1
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SGTCETFSKCWISMIWTSETDSMGSLTVDIGNDEGKCRTYRARGLLLCSKSITSISQ
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DDEHRKRSGKQKEKRKVEDIDKKKEDEKLKQEEKKRNDEDKRPDKKDEFDGKYECVAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PMSHEAFGWOTLSYKIISRLSEQMNSLVFLLWGKHARKLSYLIDAQKHLVLESAHPSP
KVKAARMPFIGCNHFVRTNLFLTEHGKDPINWNILNE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MALLQWMLDHVQDEEKNYENLSIDDQHSLFGINRDWLSFLQLSK
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LAFGTVKECSIPESLKNIFKELERSIPNFSPPDNGCLNSWCREGVLLLNSIFTVVHGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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/db_xref="GI:2769718"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/transl_except=(pos:9838.
/product="H80"
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VNGAVEGALSPCVSIDNHEDQQHDELDKRVYAQVGGVLGSPKPRSLESLLCVSKADLF
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/note="similar to HHV6A U79, HCMV UL112, spliced in vitro
/note="similar to HHV6A U79, HCMV UL112, spliced in vitro
/replication protein"
                                                                                                                                                                                                                                                 TGVEFDLLKQMEAYNSKLPFRSSRPTILIRNT"
                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/product="glycoprotein L"
/protein_id="AAC40331.1"
/db_xref="GI:2769719"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAC40329.2"
/db_xref="GI:7687902"
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/db_xref="GI:2769716"
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                                                                                  4.6%;
                                                     Score 106.4;
Pred. No. 2.5e
0; Mismatches
                                                        0
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                                                                            4; DB 72;
?.5e-07;
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                                                        166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HCMV UL114, HVS gene 46, UL2"
                                                                                                          Length 30752;
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                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gccagccgagagcccatcggagaccccaggccccagcccggcaggacctacaagggatga 1931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9ccagccgagagcccatcggagaccccaggcccccgcccggcaggacctgcaggggacga 1691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCAGCAGAGCCTCCAGCAGAGCCTCCAGCAGGCCTCCAGCAGGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Direct Submission
Submitted (18-DEC-1998) to the DDBJ/EMBL/GenBank databases.
Submitted (18-DEC-1998) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (E-mail:lsegawa@micro.med.osaka-u.ac.jp, Tel:81-6-879-3323, Fax:81-6-879-3329)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Virol. 73 (10), 8053-8063 (1999)
99412319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Comparison of the complete DNA sequences of human herpesvirus 6 variants A and B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isegawa,Y., Mukai,T., Nakano,K., Kagawa,M., Chen,J., Mori,Y.,
Sunagawa,T., Kawanishi,K., Sashihara,J., Hata,A., Zou,P., Kosuge,H.
and Yamanishi,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human herpesvirus 6 (strain: HST, pop_variant: B) DNA.e.
Human herpesvirus 6
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isegawa,Y.
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                                                                                                                                                                                   complement(18. .365)
/gene="LT1"
                                                                                                                                                                                                                                      complement(18.
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/codon_start=1
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/pop_variant="B"
                                                                                                                                                                                                                                                                                                                                                                                           /virion
                                                                                                                                                    'note="52.5% identical
                                                                                                                                                                                                                                                                                                                                                          strain-"HST"
                                                                                                                                                                                                                                                                                                                                                                                                             ∕organism="Human herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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/gene="DR6"
5025.
6512. .7150
/gene="DR7"
                                                                                                                                                                                                                                                                       complement(5023.
/gene="DRHN1"
complement(5023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="mSRVFSCVLRACVCAGLCCWVCMGVICGDCQRWWRRRCARWGRVGRVLDGGAMRVRSGDGVRSVSRTCKTERAPSAARSPVYSPPFVLVSSSSSSSSSSSACSSACSSRVDSPPPSPHAASHAVCAEGGRDLPMHGADGDADEGTDGTLLEKGGADEGAGGNAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="mrvsepthcsgfhaahpslswligsspwlvllqapggslfchdv
fggrlyllshyslflktglagceaitraplwrvrplpslwtgdddtart
arrglaaftalwrlhigsrselshpvlewertelvltdrrrwdcthllsgsgfgros
ssdagdtwnaaiekaaggkeeaerggropatdrlasphltrglrdsgrelgeepsa
edfarcrplldelcgeggwlpfafltasphvclilteggpvlaldlndtslwrladdl
ellergslllleggrelpfafltasphvclilteggpvlaldlndtslwrladdl
ellergslllliggerpsgsseaarkeggekeeggraatasatasatartsprrpt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="DR2"
1027. .2970
/gene="DR2"
                                                                                                                                                  /note="84.5% identical to DR6 HHV-6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(2718. .3320)
/gene="DR3"
                                                                                                                                                                                                                                                                                                                                                                                  /gene="DRHN1"
/note="ORF unique to HST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCPEDTRGFARSPGDLMGEMNGDLGDEGETGEGGDNGEGE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(2718. .3320)
/gene="DR3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSPLSPPSPVSPSSPRSPFISPIRSPGLRAKPRVSSGHPVAFPPAPSSAPPFSKRVPS
VPSSASPSAPCIGRSRPPSAGTA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPROVTEKGRVTTGDVPFSAHPESEEQTDGHHGRQESGHGDQRGGDGRGHRDDGARH
ANDETEPQQRGEHEDGEQTDSGREEDAQESEVARRDEKGTEQGSGRSCGRAKQTYGG
RGEHGAWSSI FLSVPREDFRVWVPPEPHLLFPSPLPSITPVEDEPSARRPCPPGGAEE
SKCSPCPPCPSPDAPQSAVPRLSALSVPSPSTARVRFSLSSLSSSSSSSSSSSSSSSSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MPLPARVSHALHRLPLSHYWWLLLGRHSLRHVHSYLRLHKGLRL PLPWPEQECLHLHPKPYKFLLRYPCLTROPHLLQGWPADSSLCE" 1027 . 2970
                                                                                                                                                                                                                                                             PSSACVALS"
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576. .842
                                                                                                                                                                                                                                                                                                                                                                          /codon_start=
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/db_xref="GI:4995981"
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/db_xref="GI:4995980"
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/db_xref="GI:4995979"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="DR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="86.4% identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .842
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                                                                                                                                                               gene of strain U1102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="BAA78218.1"
/protein_id="BAA78218.1"
/db_xref="G1:4995985"
/translation="MLAPPTPRGVYIKGECGALSSSPDLCDSPCRVGIGRCYSNSARG
/RRCLTDRRYVFFLLCGVSNTERRHIVCDCVHSFILFLIGLKAGRDTVFRTYTHPTHTR
RRIDISTAVLLEFLFLRHTPHFFFFFVLYFEILVMIFLRSCLWPYIASLRLRRGV"
7928. 8662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /928. .8662
/gene="DR8"
                                                                                                HTKKYTHTKKYTHTKKYTHKKIHTHKKIHTHKKIHTKKNHFIYALFSQC"
complement(9467. .10768)
/gene="U2"
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                                                                      complement(9467. .10768)
/gene="U2"
                                                                                                                                      /protein_id="BAA78221.1"
/protein_id="BAA78221.1"
/db_xref="G1:4995988"
/translation="MERAPREAIDLSTDPRPISVMQIRTRTRTDMPTRPHRADCHVSE
/translation="MERAPREAIDLSTDPRPISVMQIRTRTRKTHTQKNTHTQKNTHTQKNT
SIHTHEKIHTRKYTQENTHTQKYTHKK
                                                                                                                                                                                                                                                                                                                   complement(8292. .8807)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(8292.
/gene="LJ1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(7236. .7706)
/gene="DRHN2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MAAARLCRLASNUTEFARRGLQRDPVAYEEDLELPDRRMCGTNV RLFDVIAAAADEHDLLTVGGLCQTHACVSCELLETVRDPWTAVGVRWTLTVARAQY RLWPDARRQLALHLYAAHFLGPWIVCAVLSREETQTPSPPIGSGGVTLGUVPTPGPR EVETAWVIVTWRDRCYRSGPITARSAVWRTRSPPCGGWAAGHERTLDVFGPG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="transactivator"
/protein_id="BAA78217.1"
/db_xref="GI:4995984"
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/codon_start=1
/protein_id="BAA78222.1"
/db_xref="GI:4995989"
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/codon_start=1
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/function="transforming activity"
/note="42.2% identical to DR7 gen
                                                                                                                                                                                                                                               /gene≖"U]
                                                                                                                                                                                                                                                                                                        GLGLGLGLGL'
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                                                                                                                                                                                                                                                                                                                                                                                                                        note="16.6% identical toLJ1"
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                                                         'note="92% identical
                                                                                                                                                                                                     codon_start=1
                                                                                                                                                                                                                                  'note="25.6% identical to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="13.6% identical to
                                          gene family"
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KEYWORDS
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AF157706/c
LOCUS
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ACCESSION
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                     AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129245 TCCAGCAAAGCTTCCAGCGGAGTCTCTAGCAAAGCTTCCAGCAGGGCCTCCAGAAGAGCC 129186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129305 TCCAGCAGGGCCTCCAGCAGGGCCTCCAGCAGAGCCTCCAGCAGGGCGTCCGGTAGGGCT 129246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1572 tacccctgggagcccatcggagaccccaggcccagcaggacctgcaggggacga 1631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF157706.162114 bp DNA
Human herpesvirus 6B strain 229,
AF157706 L13162 L14772 L16947
AF157706.1 GI:5733510
95074921
3 (base
                                                                                                                                                                                                                                        A strongly immunoreactive virion protein of human herpesvirus 6 variant B strain Z29: identification and characterization of the gene and mapping of a variant-specific monoclonal antibody reactive
                                                                                                                                                                                                                                                                                                                                                                                                Human herpesvirus 6B
Viruses; dsDNA viruses,
                                       suggests acquisition of oriLyt b
J. Virol. 69 (1), 589-596 (1995)
                                                                                                           Stamey, F.R., Dominguez, G., Black, J.B., Dambaugh, T.R. Pellett, P.E.
                                                                                                                                                                                                    Virology 195 (2), 521-531 (1993)
                                                                                                                                                                                                                       epitope
                                                                                                                                                                                                                                                                                                              Betaherpesvirinae; Roseolovirus.

1 (bases 19696 to 22886)

Pellett, P.E., Sanchez-Martinez, D., Dominguez, G., Black, J.B., Anton, E., Greenamoyer, C. and Dambaugh, T.R.
                                                            Intragenomic linear amplification suggests acquisition of orityt by
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human herpesvirus 6B.
                                                                                                                                                        (bases 64106 to 84963)
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LPVTLPLSFFFFFILLIISRIPHRKKMFCRSPFLGISSWSLASAALCPSSCSFSAGRD
LRCDAAVPEVKWTAFVETLVARPLSADDVRDDVSTFAHCRLALSMPYGAELERATSDM
LGITQAELAKLSRGYGCCPGMDLTVIGVTIFAEVSALVLVGEGEIYAFNGVFDDALY
RLAEDAFGLWKHGLTRFEPVYGSKCLMETGASFFGGWSGVDDALAFAVSEDKALPPLP
MPRGAFFEFAVPRRAEKRWILIPGGGVAVVIGRFFGRGVTLPLLRRQRVLMDQVGRVY
AASLDGGAVVRLSDSFRAFLAWGVRKLFKNHRFPFGHLWTMQLFVTCVHAPVINLPAV
YQLSPHMVEREMSAVSCGASTVVRRDCEDTLRDGDAGVDTS"
Complement(10891...12051)
/gene"U3"
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                                                                 transposition
                                                                                      of human herpesvirus
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                                                                                                                                                                                                                                                                                                                                                                                                       Herpesviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genome
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(bases 64106 to 84963; 106012 to 126166)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                   GA 30333, USA sequence updated by submitter Sequence updated by submitter On Aug 16, 1999 this sequence version replaced g1:405170 g1:405156 g1:305397.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (10-JUN-1999) Herpesvirus Section, Centers for Control and Prevention, 1600 Clifton Road, Mailstop G18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GA 30333, USA
9 (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-OCT-1993) Herpesvirus Section, Centers for Control and Prevention, 1600 Clifton Road, Mailstop G18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (26-JUL-1993) Herpesvirus Section, Centers for Disease Control and Prevention, 1600 Clifton Road, Mailstop Gl8, Atlanta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human herpesvirus 6B genome sequence: coding content and comparison with human herpesvirus 6A J. Virol. 73 (10), 8040-8052 (1999) 99412318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lindquester,G.J., Greenamoyer,C.A., Anton,E.D., O'Brian,J.J., Pellett,P.E. and Dambaugh,T.R.
Comparison of a 20 kb region of human herpesvirus 6B with other human beta herpesviruses reveals conserved replication genes and adjacent divergent open reading frames

Arch. Virol. 142 (1), 193-204 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pellett, P.E., Dominguez, G., Dambaugh, T.R., Stamey, F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GA 30333, USA
8 (bases 64106 to 84963; 106012 to 126166)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lindquester,G.J., O'Brian,J.J., Anton,E.D., Greenamoyer,C.A., Pellett,P.E. and Dambaugh,T.R.
Genetic content of a 20.9 kb segment of human herpesvirus 6B strain 229 spanning the homologs of human herpesvirus 6A genes U40-57 and containing the origin of DNA replication
Arch. Virol. 142 (1), 103-123 (1997)
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Dominguez,G., Dambaugh,T.R., Stamey,F.R.,
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Arch. Virol. 141 (2), 367-379 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pellett, P.
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            Human herpesvirus 6 (strain Uganda-1102).
Human herpesvirus 6 (strain Uganda-1102)
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Uganda-1102) IE2hom mRNA,
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              Herpesviridae;
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1681 gcaggggacgagccagccgagagcccatcggagaccccaggccccagcccggcaggacct 1740

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CAAGCAAAGCCTCCAGCAGAGCCTCCAGCAGAGCCTCCAGCAGAGAGCCTCCAGCAGGGATT

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Virologie, Universitaet Erlangen-Nuernberg, Schlossgarten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soergel,A., Schiewe,U., Fleckenstein,B. and Neipel,F. Identification of an human herpesvirus-6 transcription unit homologous to the immediate-early 2 gene of human cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 4742)
Soergel, A., Schiewe, U.,
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SNESGSTQVRRASELENQLLQPMYTSHRQNANLQNNFTSLPXQPYXDIESSYRE
SRNYNRGYDYNERHHYYRPRGGURKYNYYNPAKKYQQPYKRCETRTYNRGRGHRXYD
CSDRSADLPYEHYTYPNYEQQNPDPRMNNYKDFTQLTNKFNFESYDYSMAFSTDSTHV
                                                                                                                                                                PNITYSEAFKMNHAPPKYYDKDEIKRFIQLQKQGPQELWDKFENNTTHDLFSRHSDYK
TMIIYAATPIDFYGAVKTCNKYAKDNPKEIVLRYCSIIDGDNPISIYNPISKEFKSKF
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FDDLIIPGLESFGLIIPESSNNIESNNVEEGSDGELKTLAEQKCKQGNDNDVIQSAMK
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/protein_id="AAB67722.1"
/db_xref="GI:2343283"
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/db_xref="taxon:10370"
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Score 92.2; DB 72;
Pred. No. 6.9e-05;
0; Mismatches 178;
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AF015298
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                                                                                                                                                                                                                                                                                                                                                                                           Erlangen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soergel.A., Schiewe, U., Fleckenstein, B. and Neipel, F. Identification of an human herpesvirus-6 transcription homologous to the immediate-early 2 gene of human cytomegalovirus--evidence for an early/late gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Betaherpesvirinae; Roseolovirus.
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                                                                                                                                                                                                                            /product="IE-2 protein"
/protein_id="AAB69858.1"
/db_xref="GI:2384715"
                                                                                                                                                                                                                                                                                                                           /organism="Human herpesvirus
/strain="Uganda-1102"
/db_xref="taxon:10368"
                                                                                                                                                                                                                                                                            join(1846. .1904,1993.
/gene="ie2hom"
                                                                                                                                                                                                                                                                                                 /gene="ie2hom"
                                                                                                                                                                                                                translation="mepakpsgnnmgsndermqdyrpdpmmeesikeileeslmcdts/
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RESULT 15
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U13194
        Center,
                                                                                                    major immediate-early and replication genes Virology 204 (2), 738-750 (1994) 95027704
                                                                                                                                                                                                                                                                                                                                                                          (HDLF1), putative helicase (HDRF2), putative phosphoprotein (EDRF1), replication protein (EDRF2), putative uracil-DNA glycosylase (EDLF4), putative glycoprotein (EDLF3), putative glycoprotein (EDLF3) genes, complete cds, and major immediate-early protein (EDLF0) gene, partial cds.
                          Submitted
                                             Direct Submission
                                                                                                                                                                                                                                       Human herpesvirus 6.
Human herpesvirus 6
Viruses; dsDNA viruses, no RNA stage;
Betaherpesvirinae; Roseolovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HHU13194 21191 bp DNA VRL 17-JUN-1995
Human herpesvirus 6 replication origin-binding protein (HDRFO),
partial cds, helicase-primase component (HDRFI), virion protein
                                                               Nicholas,J
                                                                                                                                                                                                    Nicholas, J.
                                                                                                                                                                                                                                                                                                                                         U13194.1 GI:862477
                                                                                                                                                         Nucleotide sequence analysis of a 21-kbp region of the genome of human herpesvirus-6 containing homologues of human cytomegalovirus
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ed (09-AUG-1994) John Nicholas, Johns Hopkins Oncology
Johns Hopkins University, 418 North Bond Street, Balt
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KRISGAQKTESEYSEEDDLCYEBYYKLKERKYSEKFKHHRGVATKDFQKLFRNTMRA
FEYKQIPKKPCNEKNLKEAVYDICCNGLSNNAAIIMYFTRSKKVAQIIK MQKELMIK
PNITVSSAFKMHAPFXYYDKDEIKRIJOLOKOGPQELWDKFENNTTHDLFSRHSDVK
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Pred. No. 4.3e-05;
D; Mismatches 178;
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complement(939. .4721)
/gene-"HDLF2"
/gene-"HDLF2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="HDRF1"
/note="component of helicase-primase complex; similar HCMV UL102 Swiss-Prot Accession Number P16827"
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complement(3972...4721)
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1949. .3937
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RKQTIYKLQGSDISLSVSEVGVFGQHASPGVCVSS"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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                           gene
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GLVNDGLSDVDLLEIDPCGDPFFTRYSKLPLTNSLSFEEISLLYTTFKDIFISRFAIL
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P16735"
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Search completed: October 12, 2000, 17:23:38 Job time: 32794 sec
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Best Local Similarity 53.3%;
Matches 176; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19431 TCCAGCAGAGCCTCCAGCAGGGATTCTAGCAGAGCCTCCAGCAGAGCCTCCAGCAGGGAT 19372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19491 CCCAGCAGAGCCTCAAGCAGAGCCTCCAGCAGGGATTCTAGCAGGGCATCAAGCAGAGCC 19432
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                                                                                                                                                                                  cccggcaggacctacaagggatgagccagc 1937
                                                                                                                                                                                                                                                              TCCAGCAGAGCCTCCAGCAGGGATTCTAGCAGAGCCTCCAGCAGGGATTCTAGCAGGGAT 19192
                                                                                                                                                                                                                                                                                                              cccggcaggacctgcaggggacgagccagccgagagcccatcggagaccccaggccccag 1907
                                                                                                                                                                                                                                                                                                                                                                                    TCCAGCAGAGCCTCCAGCAGAGCCTCCAGCAGGGATTCTAGCAGGGCCTCAAGCAAAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cccggcaggacctacaagggatgagcccagccgagagcccatcggagacccccaggcccccg 1787
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Swiss-Prot Accession Number P17151"
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Accession Number P16768"
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12483. .131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 83.6; DB 72;
Pred. No. 0.00065;
0; Mismatches 154;
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Title:
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

REFERENCE AUTHORS TITLE JOURNAL COMMENT

ISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

NRS NIH-MCC http://www.ncbi.nlm.nih.gov/MGC/.

NATIONAL Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be http://image.llnl.gov

Plate: LLAM8545 row: f column: 19

High quality sequence stop: 552.

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Plate: LLAM8545 row: f column: 19

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FEATURES

source

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

EST.

house mouse.

mRNA sequence. BE282484 BE282484.1 GI:9158085

82182484 654 bp mRNA 657 601103075F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3495186 5',

LOCUS DEFINITION

SUMMARIES

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3343 343 313 314 414 322 1296 559	44 44 44 44 44 44 44 44 44 44 44 44 44	432 402 402 419 412	443 480 420 363 418	654 590 735 500 500 500 506 868 868 522 522 522 522 522 523 524 729 729	Length
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AV168 A0087 A0717 AW326 AW323 AW323 BE409 C8149 AW631	W2507 16277 17141 17606 24820		41358 41358 07852 76372 76372 73593	BE282484 AII15047 BE534864 AII173869 BE288040 AW7526644 AW321684 AW476433 AI786854 BE277227 AW538283 AI578564 AL120919 AW251730 AW251730 AW358283 AI578564 AL120919 AW251730 AW358283 AI578564 AI120919 AW251730 AW358283 AI578564 AI120919 AW251730 AW358283	ID
750 01-K-08888516 AVV188738 mg98f0768 mm70h06593 193806593 193809569 601299569 60129	0708 2822396 771 mn43d06. 4165 UI-R-AG 06 EST105106 2073 167730	.89 au45h07 .89 au45h07 .89 au45h07 .891 6013033 .87 me27e10 .87 me50h02 .9 mo50h02 .9 ue09b05 .0 ui41f12	7153 0012/00 13582 EST02485 7852 EST02485 3727 ur64h02 3727 EST105107 247 EST105107	82484 60110301 5047 W141f12) 34864 6012314 34864 6012314 3869 we92f06) 88040 6010947 62644 wr64h02 271684 wo37c01 76433 wg75g05 76433 wg75g05 76564 W1-R-AMO 2019 DKFZp762 51730 W1-R-AMO 51730 W1-R-A	Description

BASE COUNT ORIGIN

179 a

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/db_xref="taxon:10090"
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/clone="IMAGE:3495186"
/clone=lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary.
/tissue_type="spontaneous tumor, metastatic to mammary."
/tissue_type="spontaneous tumor, metastatic tumor, metastatic tumor, metastatic tumor, metastatic tumor, metastatic tumor, metastatic tu

ALIGNMENTS

RESULT BE282484

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532 cgggaaccaggagtgaactggcacgccaagcccctcaccctgaaggaggttgaggcattt 591	306 AAAGACAACTATGACCTCCTGGAAGAGAATCACTCCTACATCCAGTGGCTGTTTCCCCTG	246 AAAATGAGATCTGCTTCCAGCCAGATGGCTTTCTCATTGAGGACATTCTTCAGAACTGG	412 aaaaatgagatctgcttccagccaaatggggctctc	292 126 352 186				232 gatgaggacacgggcgacgatgacggcgacgcgga			Query Match 25.4%; Score 572; DB 34; Best Local Similarity 94.4%; Pred. No. 9.3e-116; Matches 593; Conservative 0; Mismatches 35;		
caccctgaaggaggttgaggcattt 591	CTACATCCA9t99ct9tttcctctg 531	CATTGAGGACATTCTTCAGAACTGG 305	catcgaggacattcttcagaactgg 471		tgacatgtgcaacctgagcttctac 411	GCAGGACATGCAAAGATACCGGCAC 185	gcaggacatgcaaagataccggcac 351		Nggaggcacggccaagcctgttccag 291	ACGATGGCCAGGCGGATGATACGACC 65	ggatggccaggcggatgatacgacc 231	es 35; Indels 0; Gaps	DB 34; Length 654;

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Gaps

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REFERENCE
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u141f12;y1 Sugano mouse embryo m
IMAGE:1885007 5', mRNA sequence.
AII15047
                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 314 286 1810
Email: mouseestewatson.wustl.edu
Emis clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further j
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 590)
MARTA,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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AI115047.1 GI:3515371
EST.
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                                                                                                                                                                                                                                                                                                                                                                     primer: custom primer used quality sequence stop: 531.
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314 286 1810
                                                                                                                                                                                                                                                                                                                                                   quality sequence stop: !
Location/Qualifiers
/note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
Site_2: DraIII (CACCATCTG); 1st strand cDNA was primed
with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[TGTTGGCCTACTGG], digested and cloned into distinct DraIII
sites of the pME18-FL3 vector (5' site CACTGTGTG, 3' site
CACCATGTG). MoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed by Dr. Sundo Sugano
(University of Tokyo Institute of Medical Science).
Custom primers for sequencing: 5' end primer
CTTCTGCTCTAAAAGCTGCG and 3' end primer
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eutheria;
                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gagaatcactcctacatccagtggctgtttcctctgcgggaaccaggagtgaactggcac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGTCTTGTCCGGGCCTATGAGCTCATGCTGNGCTTCTATGGGATCCAACTTGAGGACCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCAAGCCCCTCACACTGAAGGAGGTTGAGGCATTTAAAAGCTCCAAGGAAGTCAGAGAG
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies,
cDNA Library Arrayed by: The I.M.A.G.E. Consc
DNA Sequencing by: Incyte Genomics, Inc.
                                                                                                                      NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 735)
                                                                                                                                                                                                                                                                                                                                 BE534864 735 bp mRNA
601231408F1 NCI_CGAP_Mam6 Mu
                                                                                    Contact: Robert Strausberg,
Tel: (301) 496-1550
                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                   mRNA
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95.5%;
                                                                                                                                                                                          Chordata;
Rodentia;
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Pred. No. 3.6e-109;
0; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                   Mus
                                                                                                      Ph.D
                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                   musculus
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                                                                                                                                          Gene
                   Consortium
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09-AUG-2000 IMAGE:3595608

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675

487

427 555 367 495 307 435 247 375 187

(LLNL)

FEATURES

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Query Match
Best Local S
Matches 595
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                                                                                                                                                                                                                                aaagctccaaggaagtcagagagcgtcttgtccgggcctatgagctcatgctgggcttct
            TCAAGTCGCTGGGCGAGCTGGGCTTAG
                              tcaagtcactgggtgagctgggcttag 796
                                                                         CCACGCTTCCACAGATCTCAACAGCCACAAGCCACAACCAATCTGCGTATTACACGCAT-C
                                                                                            ccgcgcttccaca-atctgaacagccac-agccacaacaacctgcgtattacacgcatcc
                                                                                                                                           ATGGGATCCAACTTGAGGACCGGAACACAGGCGCCGTATGCCGTGCACAGAAACTTCCAG
                                                                                                                                                            atgggttccaccttgaggaccggggcacgggtgctgtatgccgtgcacag-aacttccag
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                                                                                                                                                                                                                                                                                GGGAACCAGGAGTGAACTGGCATGCCCAAGCCCCTCACACTGAAGGAGGTTGAGGCATTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                 AAATGAGATCTGCTTCCAGCCAAATGGCTTTCTCATTGAGGACATTCTTCAGAACTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                      aaatgagatctgcttccagccaaatggggctctcatcgaggacattcttcagaactggaa 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTACCCGGATTTGACAGATCAAGACTGCAACGGAGACATGTGCAACCTGAGCTTCTACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ctacccggatttgacagatcaagactgcaatggtgacatgtgcaacctgagcttctacaa 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAGGATGACAAGGTACCGAAACTGGCGTGCTATGCAGGACATGCAAAGATACCGGCACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          caggatgacagggtaccgaaactggcgtgctatgcaggacatgcaaagataccggcacaa 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGAGGACACGGGGACGACGCGACGCGAGGGAGGCACGGCCAAGCCTGTTCCAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tgaggacacgggcgacgatgacggcgacgcggagggaggcacggccaagcctgttccagtc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    il Similarity
595; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM8771 row: o column: 01
High quality sequence stop: 621.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IINAGE:3595608"
/clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
a 196 c 214 g 131 t
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Pred. No. 3.9e
0; Mismatches
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3.9e-105;
hes 27;
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AUTHORS
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KEYWORDS
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AI173869
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                                                                                                                                                                         Matches
                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                     196
                                                                                                                                         136
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Mammalia; Eutheria;
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                                                                                                                                                                       Conservative
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BASE COUNT ORIGIN

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                           9909acgcggaggcacggccaagcctgttccagtccaggatgacagggtaccgaaac
                                                                                                                                 gaggatggcgaggatggccaggcggatgatacgaccgatgaggacacggggcgacgatgac
GGCGACGCGGAGGCACGGCCAAGCCTGTTCCAGTCTAGGATGACAAGGTACCGAAAC
                                                                                                      GAGGACGCCAGGCCAGGCGGATGATACGACCGATGAGGACACGGGCGACGATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae 1 (bases 1 to 564)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuc Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI173869 564 bp mRNA ue92f06.y1 Sugano mouse embryo m IMAGE:1498595 5', mRNA sequence. AI173869 GI:3720011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: custom primer used High quality sequence stop: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[TGTTGGCCTACTGG], digested and cloned into distinct DraIII
sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
CACCATGTG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed by Dr. Sunio Sugano
(University of Tokyo Institute of Medical Science).
Custom primers for sequencing: 5' end primer
CGACCTGCACCACCACA."

CGACCTGCACCACCACA."

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/clone="TMAGE:1498595"
/clone_lib="Sugano mouse embryo mewa"
/dev_stage="embryo, 14 dpc"
/lab_host="DH10B"
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Location/Qualifiers
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Rodentia;
                                                                                                                                                                                                                                                                                                                       Score 519.6; DB 9;
Pred. No. 3.1e-104;
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                                                                                                                                                                        Email: Robert_Strausberg@nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphr
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8530 row: c column: 07
High quality sequence stop: 661.
Location/Qualifiers
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NIH-WCC http://www.nobi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian (Unpublished (1999)
                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse
                                                           /organism="Mus musculus"
/strain="C57/B6"
/db_xref="taxon:10090"
/clone=".mAGE::489342"
/clone_lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stagep="7 months"
/lab_host="DH10B"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Murid
1 (bases 1 to 500)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                       AW762644 500 bp mrNA EST 04-MAY-2000 ur64h02.y1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:3155091 similar to TR:096029 096029 7-60. ;, mrNA sequence.

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cgtcttgtccgggcctat
                          GCCAAGCCCTCACACTGAAGGAGGTTGAGGCATTTAAAAGCTCCAAGGAAGTCAGAGAG
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                                                                                                                                                        AATGGCTTTCTCATTGAGGACATTCTTCAGAACTGGAAAGACAACTATGACCTCCTGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: Robert_Strausberg@nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
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Location/Qualifiers
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/clone_11b="NCI_CGAP_Mam3"
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/strain="129 - C57/B6 -
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Pred. No. 1.7e-93;
0; Mismatches 17
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High
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Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalia; Eutheria; Rodentia; Sciurognathi; M
1 (bases 1 to 506)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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Contact: Robert Strausberg,
Tel: (301) 496-1550
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h quality sequence stop: '
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
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/clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                          /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"

125 c 149 g 91 t
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Rodentia; Sciurognathi; Muridae;
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Pred. No. 9.6e-92;
0; Mismatches 22;
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                                                                                                                                                                                                                                   MGI:1049404
Seq primer:
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                      Email: Robert_Strausberg@nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA_Library Preparation: M. Bento Soar
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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/db_xref="taxon:10090"
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                              uj32d09.yl Sugano mouse kidney mkia
IMAGE:1921649 5', mRNA sequence
A1786854
                                                                                    Unpublished (1999)
Other_ESTS: uj32d09.x1
Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                           Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylle,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                               Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                       Eukaryota;
Mammalia;
                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                             nouse mouse
                                                                                                                                                                                                                                                                                      AI786854.1
                                                                                                                                                                                                       karyota; Metazoa;
mmalia; Eutheria;
(bases 1 to 447)
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314 286 1810
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Matches 422; Conserv
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                             BE277227 868 bp mRNA F
601178592F1 NIH_MGC_20 Homo sapiens cDNA
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Seq primer: custom primer used High quality sequence stop: 434
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/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1921649"
/clone_lib="Sugano mouse kidney mkia"
/sex="female"
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Pred. No. 1.6e-80;
0; Mismatches 17;
                             EST 13-JUL-2000 clone IMAGE& 3050950 5',
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Best Local Similarity 76.8
Matches 547; Conservative
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                    ggctctcatcgaggacattcttcagaactggaaagacaactatgacctcctggaagagaa
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TGTCCGGGCCTACGAGCTCATGCTGGGCTTCTACGGGGATCCGGCTGGAGGACCGAGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM97 row: h column: 23 High quality sequence stop: 742.

Location/Qualifiers
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NIH.MGC http://www.ncbi.nlm.nih.gov/MGC/.
NIH.MGC http://www.ncbi.nlm.nih.gov/MGC/.
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 National Institutes of Health,
Unpublished (1999)
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Mammalia; Eutheria;
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/db_xref="taxon:9606"
/clone="IMAGE:3050950"
/clone=lib="NIH_MCC_20"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lote="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into ECORI/NoI Sites using the following 5' adaptor: GCCAGCGG(S). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA, synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
71 a 245 c 294 g 157 t 1 others
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Procurement: ATCC/DCTD/DTP
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76.8%;
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Pred. No. 1.8e-76;
0; Mismatches 154;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 508)
1 (bases 1 to 508)
Tanaka, T.S., Jaradat, S.A., Lim, M.K., Kargul, G.J., Wang, X., M.J., Pantano, S., Sano, Y., Piao, Y., Nagaraja, R., Doi, H., W III, Becker, K.G. and Ko, M.S.H.
Genome-wide expression profiling of mid-gestation placenta embryo using a 15,000 mouse developmental cDNA microarray Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
Contact: George J. Kargul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW538283 508 bp mRNA EST C0105F08-3 Mouse E7.5 Extraembryonic Portion CDNA musculus CDNA clone C0105F08 3', mRNA sequence. AW538283 GI:7180700 EST. house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cdna@lgsun.grc.nia.nih.gov
Plate: C0105 row: F column: 08
Seq primer: -21M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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from 0.8ug of mRNA. The double-stranded cDNAs were treated with 74 DNA polymerase and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal3 (include Sal1 sequence). The cDNAs were purified by phenol/chloroform and separated from free linkers by Centricon 100. Then, cDNAs were amplified by long-range high fidelity PCR using Takara's Ex Taq
                                                                                                                                                                                                            /sex="unknown"
/dev_stage="7.5dpc Embryo"
/lab_host="DH10B"
/nab_host="DH10B"
/note="Vector: psPoRT1 (Gibco/BRL Life Technology);
Site_1: Sall; Site_2: Not1; Total RNAs were extracted from 5 EPC. The double-stranded cDNA was synthesized by
                                                                                                                                                                                        Gibco's kit with an Oligo(dT) primer [NotI primer-adapter
                                                                                                                                                                                                                                                                                                                                            Library
                                                                                                                                                                                                                                                                                                                                                           /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="C0105F08"
/clone_1ib="Mouse E7.5 Extraembryonic
                                                                                                                                             from GibcoBRL
                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
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Wood, W.H.
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Local Similarity 90.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGCCTTCAGAAGCCTCCTTACCTCACTGTG----TCCTCCACTGCCCTCTGAGCCCTGTG
                                                                                                                                                                                                                                     AI578564 403 bp mRNA EST 05-APR-1999 UI-R-AA0-wl-g-01-0-UI.sl UI-R-AA0 Rattus norvegicus cDNA clone UI-R-AA0-wl-g-01-0-UI 3', mRNA sequence.
Genome Res. 6 (9), 97044477 Contact: Soares, MF
                                                                                                                                           Rattus norvegicus
Eukaryota; Metazoa;
                                                                         1 (bases 1 to 403)
Bonaldo, M.F., Lenno
                                                  discovery
                                                            Bonaldo,M.F., Lennon,G. and Soares Normalization and subtraction: two
                                                                                                              Rattus
                                                                                                                               Mammalia;
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                                                                                                                                 Eutheria;
                                                                                                                                                                                                              GI:4562940
                                 791-806 (1996)
                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 391.8; DB 22;
Pred. No. 4.1e-76;
0; Mismatches 42;
                                                                              and Soares, M.
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                                                                                                                 TCAGACCCTAAGGGTCTAGAGGGAGGGGCCTCTTCATTAGTCTGGTGCCCAAGTGAGGCCT
                                                                                                                                                                                        tcagaccctaagggtctagagggaggggctcttcattagtctggtgccaagtgaggcct
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             AL120919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: msoares@blue.weeg.uiowa.edu
The Sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
non-normalized atrium at 16.5 dpc library cDNA Library Preparation:
M.B. Soares Lab Clone distribution: clones will be available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8256
Fax: 319 335 9565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  through Research Genetics (www.resgen.com) Seq primer: M13 Forward.
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/norte="Vector: pT773D-Pac (Pharmacia) with a modified
/norte="Vector: pT773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not 1; Site_2: Eco RI; The UI-R-AAO
library is a non-normalized library constructed from 16.5
dpc rat atrium. The tag is a string of 5 nucleotides
present between the Not I site and the oligo-dT track.
The library was constructed as described by Bonaldo,
Lennon and Soares, Genome Research 6: 791-806, 1996.
Tissue provided by Jim Lin, Department of Biology,
University of Iowa."
99 a 107 c 105 g. 92 t
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/strain="Sprague-Davley"
/db_xref="ttaxon:10116"
/clone="UI-R-AAO"
/clone_lib="UI-R-AAO"
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Pred. No. 4.5e-75;
0; Mismatches 10;
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gaacagccacagccacaaccagcctgcgtattacacgcatcctcaagtcactgggtgagct
                                                          99acc9999cac999t9ct9tat9cc9t9caca9aacttcca9ccgcgcttccacaatct
                                                                                                       CCAGGAGCGGCTTGTCCGGGGCTACGAGCTCATGCTGGGCTTCTACGGGATCCGGCTGGA
                                                                                                                            cagagagcgtcttgtccgggcctatgagctcatgctgggcttctatgggttccaccttga
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                                   GGACCGAGGCACGGGCACGGTGGGCCGAGCACAGAACTACCAGAAGCGCTTCCAGAACCT
                                                                                                                                                                              CTGGCATGCCAAGCCCCTCACGCTCAGGGAGGTCGAGGTGTTTAAAAAGCTCCCAGGAGAT
                                                                                                                                                                                                                                                  CCTTGAGGACAATCACTCCTACATCCAGTGGCTGTTTCCTCTGCGAGAACCAGGAGTGAA
                                                                                                                                                                                                                                                                                                                         ccagccaaatggggctctcatcgaggacattcttcagaactggaaatgacaactatgacct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No sl sequence available.
This clone (DKTsp/62B143) is available at the please contact the RZPD: Ressourcenzentrum, Berlin-Charlottenburg, GERMANY; Email: clone Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by BMFZ (Biomedical Research Center at the Charite, Berlin/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Primates; Cate
1 (bases 1 to 522)
Koehrer, K., Beyer, A., Mewes, H.W.,
EST (Koehrer, et al.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Koehrer K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DKFZp762B143_r1 762 (synonym: hmel2) Homo
DKFZp762B143 5', mRNA sequence.
AL120919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL120919.1 GI:5926920
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="melanoma (MeWo
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSport1; Site_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="DKFZp762B143"
/clone_lib="762 (synonym:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Metazoa;
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83.5%;
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; Pred. No. 2.9e
0; Mismatches
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is available at the RZPD in Berlin.
Ressourcenzentrum, Heubnerweg 6, 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Site_1: 98 t
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?.9e-74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the
OligonucLeotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
normalized ventricle at 13 dpc library cDNA Library Preparation:
M.B. Soares Lab Clone distribution: clones will be available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW251730 386 bp mRNA ES
UI-R-BJO-aef-c-04-0-UI.sl UI-R-BJO Rattus
UI-R-BJO-aef-c-04-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 386)
Bonaldo, M.F., Lenno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       through Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97044477
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                                 þ
                                                                                                                                                                                            /lab_host="DH10B (Life Technologies)"
/note="Vector: pT773D-Pac (Pharmacia) with a modified
/note="Vector: pT773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BJ0
library is a subtracted library derived from the UI-R-AA1,
UI-R-AB1, uI-R-
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                                                         TAG_TISSUE=ventricle at 13 dpc
TAG_SEQ=CAGCGA"
                                                                                                                   TAG_LIB=UI-R-BJO
                                                                                                                                              6: 791-806,
                                                                                                                                                  described by Bonaldo, Lennon and 6: 791-806, 1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="Ur.R-BJO-aef-c-04-0-UI"
/clone_11b="UI-R-BJO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Rattus norvegicus"
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Query Match

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Score

377;

ВВ

21;

Length 386;

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Best Local Similarity
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AW538292
AW538292.1
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Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X., Grahova,M.J., Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Doi,H., Wood,W.H. III, Becker,K.G. and Ko,M.S.H.
Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental CDNA microarray Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW538292 529 bp mRNA EST 02-AUG-2000 C0105G09-3 Mouse E7.5 Extraembryonic Portion cDNA Library Mus musculis cDNA clone C0105G09 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cdna@lgsun.grc.nia.nih.gov
Plate: C0105 row: G column: 09
Seq primer: -21M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: George J. Kargul Laboratory of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, I
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                                                                                                                                                                                                                                                                                                                                                                                                       quality sequence stop:
                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/60"
/db_xref="faxon:10090"
/clone="C0105G09"
/clone_1ib="Mouse E7.5 Extraembryonic Portion
                                               /sex="unknown"
/dev_stage="7.5dpc Embryo"
/lab_host="DH10B"
/note="Vector: pSPORT1 (Gibco/BRL
Site_1: Sall; Site_2: NotI; Total
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BASE COUNT
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Best Local Similarity
Matches 468; Conserv
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                  2150 attagtctggtgccaagtgaggccttttctgaataaactctttagactttgtcaa 2204
                                                                                        1791 gagccctgtggaggaccctgactctgacactatgggaacctcagtggatgagtcagagga 1850
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CTTCGTCTGATGCCAAGTGAGGCCTTTTCTGAATAAACTCTTTAGGCTTTGTCTA 2
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                                                                                                                                             TGCCCTCAGGGAAGGCCAAGGCCTTCAGAAGCCTCCTTACCTCACTGTG---TCCTCCAC
                                                                                                                                                                                                                                                                                                                                                            GTTGGCAAGGATTGAGGCCTCTGTTGAACCCCCAAAGCCTTAGAGGTACCCTTCAGTCCT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAGGTGGGGTCAGAGGACCCCCAAAGCTA---GGTGGCGCTAGAGTAAGCTGCCTCTAA 413
                                                                     TGCCCTCTGAGCCCTGTGTTGTGAACAGACCCTAAGGGTCTAAGGGGATGGGCCTCTTTT 57
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Search completed: October 14, 2000, 03:41:44
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5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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Gapop 10.0 , Gapext 1.0
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    GenCore version Copyright (c) 1993 - 2000
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US-08-232-463-14
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US-08-781-891-209
US-09-130-111-1
US-09-130-114-1
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US-08-087-783A-15
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APPLICANT: DORNER, F. APPLICANT: SCHEIFLINGER, F. APPLICANT: FALKNER, F. G. TITLE OF INVENTION: RECOMB-
NUMBER OF SEQUENCES: 52
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SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US
FILING DATE:
 1092
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MEDIUM TYPE: Floppy disk
COMPUTER: IDM PC compatible
COMPUTER: DM PC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                      1182
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CLONE: pTZgpt-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                            942
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RRRRRRRRRRRRRRRRRRRRRRATCGCAAGCTCCCTCGACCTGCAGCCAAGCTCGG 1033
                       cctcaggacgggacccaggaagtgggcggtcaggaccctggggaggcctcctgtccctg 1361
                                                               gaagaggaagctggagctgagccggcgggagcagccgcccacagagccaggccctcagag 1241
                                                                                                                                                                                                                                                                                                     9999ccccagccacggagcgtggagccccaggatgcgggacccctggagaggagccaggg 1121
                                                                                                                                                                                                                                                                                                                                                                   gctcgagggctccaggaaggtggaggaaggaaggccccgggggaccccgaccacgaggc 1001
                                                                                              tgcctcagaggtggagaagatcgctctgaatttggaggggtgtgccctcagccagggcag 1301
                                                                                                                                                                                                     ggatgaggcagggggccacggggaagataggccggagcccttaagccccaaagagagcaa 1181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.5%; Score 72.8; DB : ilarity 5.5%; Pred. No. 6.8e-07. Conservative 240; Mismatches 1:
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US-07-945-283-1
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US-07-945-283-1
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                                                            Query Match 3.9%;
Best Local Similarity 67.4%;
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 309-585-4128
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8438 base pairs
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TELEPHONE: 309-685-4011 ext.513
TELEFAX: 309-685-4118
                                                                                                                                                                                  LOCATION: FEATURE:
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HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                 63
                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: NUCLEIC ACID STRANDEDNESS: doub TOPOLOGY: linear
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CITY: Peoria
                                                                                                                                                                                                                                                                                                          NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UZIP: 61604
                                                                                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                          LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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                       ggaggaggacgaggatgcggaggacgcgggaggacgaggactgcgaggacggcgaggc 122
1, Application US/07945283
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622..6495
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replace(7010, "g")
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Ronald D.
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                                                            Score 61.8; DB 1;
Pred. No. 0.00014;
0; Mismatches 42;
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Best Local :
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INFORMATION FOR SEQ ID NO: 1:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 3489 base pairs
TYPE: nucleic acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/728,323A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/52268/JPW/MSC/SKS
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1088 AGGATGACGAGGAGGATGACGAGGATGACGAGGATGACGAGGATGACGAGG
                                                                                                                                  1028 AGGATGACGAGGAGGATGACGAGGAGGATGACGAGGATGACGAGGAGGATGACGAGG 1087
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                     122 ccgccggcgcgagggacgcggaggacgagggacgaggagtcggaggagcgcgcggg 181
                                                                                                                                                                                                                                                                                                         NAME/KEY:
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STATE: New York
                                                                                    62 gggaggaggacgaggatgcggaggacgcggaggacgaggactgcgaggacgcgcgagg 121
                                                                                                                                                                                                        Local Similarity 57.0 ies 107; Conservative
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1185 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212-391-0525
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Pred. No. 0.00025;
0; Mismatches 78;
                                                                                                                                                                                                                                      Length 3489;
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FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 5234:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400:
TELEPHONE: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
TYPE: DOCUMENT OF THE PAIR ACT OF THE PAIR SECONICE CHARACTERISTICS:
LENGTH: 32207 base pairs
                                                                                                                                                                                                                                                                                                                        Query Match
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Patent No. 5849564
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20789 AGGAG 20785
                                                                     20909 AGGATGACGAGGATGACGAGGAGGATGACGAGGATGACGAGGAGGATGACGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Edelman, Isidore S. APPLICANT: Moore, Patrick S. TITLE OF INVENTION: POLYPEPTIDES TITLE OF INVENTION: HERPESVIRUS, NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                               182 cggcg
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                                                                                                                                                             62 gggaggaggacgaggaggatgcggaggacgcgggaggactgcgaggacggcggggg 121
                                                                                                                                                                                                                                                                                      Local Similarity 57.8 ies 107; Conservative
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10036
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                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                              2 agaattcagcggccgctgaattctagccgagcatggacgaccccgactgcgactccacct 61
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Russo, James J
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                                                                                                                                                                                                                                                                                                                                                                                                                                 double
                                                                                                                                                                                                                                                                                                       3.8%;
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Pred. No. 0.0004;
0; Mismatches 78;
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                                      Patent No. 6090620
GENERAL INFORMATION:
                                                       Sequence 209, Application US/08781891 Patent No. 6090620
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Best Local S
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GENERAL INFORMATION:
APPLICANT: Gold, Larry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: January 31, 1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
RAPPLICATION UMBER: 07/739,05
FILING DATE: 01-AUGUST-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (303) 850-94
INFORMATION FOR SEQ ID NO:
              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 150 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch,
COMPUTER: IBM compatible
  APPLICANT:
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CURRENT APPLICATION DATA:
                                                                                                                                                        153 cgaggacgaggagtcggagg 172
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                         65
                                                                                                                                                                                                           33 catggacgaccccgactgcgactccacctgggaggaggacgaggaggatgcggaggacgc 92
                                                                                                                                                                                                                                                                                                            Match 3.6%;
Local Similarity 63.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/07/829,461A FILING DATE: January 31, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
SOFTWARE: WORDER
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                                                                                                                                                                                                                                         CGACGCCATGGTTGCGATGG 144
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Denver
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Fu, Ying-Hui
Yu, Chang-En
Oshima, Junko
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Pred. No. 0.0003;
0; Mismatches 5
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                                                                                                                                                                                                                                                                                             51;
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                                                                                                                                                                                                                              GENERAL INFORMATION:
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 209
                                                                                                                                                                             APPLICANT: I
APPLICANT: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Mulligan, APPLICANT: Schellent TITLE OF INVENTION: TITLE OF INVENTION:
                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Te
STREET: 4 Embarcadero Center,
                                                                                                                         TITLE OF INVENTION: Mammalian Protein Interaction Cloning TITLE OF INVENTION: System NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 51259 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/00
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                            167
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                                                                                                                                                                                                                                                                                                                                            159 AGGAGGAGCAGGAGGAG 140
                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Wartle
                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 actgcgactccacctgggaggaggacgaggatgcggaggacgcggggggacgaggact 106
                                                               CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TORNEY/AGENT INFORMATION:
NAME: NO. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 9,317
REFERENCE/DOCKET NUMBER: 240052.419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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89; Conservative
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                                               CA
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Hiang, Betty
Payan, Don
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Schellenberg, Gerald D.
Schellenberg, Gerald D.
VENTION: GENE AND GENE PRODUCTS RELATED TO
VENTION: WERNER'S SYNDROME
EQUENCES: 209
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Pred. No. 0.0011;
0; Mismatches 51;
                                                                             Test, Albritton & Herbert er, Suite 3400
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; TOPOLOGY: unknown ; MOLECULE TYPE: DNA US-09-050-863-2
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NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-65
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-189
TELEPAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2580 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TORDICCY. "SECOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.6%;
Best Local Similarity 43.2%;
Matches 272; Conservative
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION UNBER: US/09/050,863
FILING DATE: 30-MAR-1998
 1291
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                                                                                                                                                                                                                                                                                          aaggtggaggaggaaggccccggggacccccgaccacgaggccagcacccagggtcgg 1017
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                                                                                                 aagatcgctctgaatttggaggggtgtgccctcagccagggcagcctcaggacggggacc
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CAGGAGCAGGAGGGCAGGAG
                          caggaagtgggcggtcaggaccctggggag 1347
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Pred. No. 0.001; 
0; Mismatches 358; Indels
1320
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Horlick, Robert A.

APPLICANT: Damed, Bassam B.

APPLICANT: Robbins, Alan K.

APPLICANT: Robbins, Alan K.

TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Gen

TITLE OF INVENTION: From Multiple Transfected Episomes

FILE REFERENCE: 0867/1D903US1

CURRENT APPLICATION NUMBER: US/09/130,114

CURRENT FILING DATE: 1998-08-06

NUMBER OF SEQ ID NOS: 36

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 1

LENGTH: 5452

TYPE: DNA

ORGANISM: VEBNA

US-09-130-114-1
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Best Local Similarity 43.2%;
Matches 272; Conservative
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                                                         tgagccggcgggagcagccgccacagagccaggcctcagagtgcctcagaggtggag
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                                                                                                                                                                                                                                                                                                                                                                                                             gigoggoagagigocolggaciaciicaigilogocgigocgolgocgacaccagogocgo 837
                                                                                   aagatcgctctgaatttggaggggtgtgccctcagccagggcagcctcaggacggggacc
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CAGGAGCAGGAGGGGCAGGAGGAGGAG
                                                                                                                 Score 57.2; DB 4;
Pred. No. 0.0012;
0; Mismatches 358;
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; Sequence 15, Application US/07884811
; Patent No. 5316921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-884-811-15
                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.6%;
Best Local Similarity 43.2%;
Matches 272; Conservative
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
1078 agogtggagccccaggatgcgggacccctggagaggagccaggggggatgaggcagggggc 1137
                                                                                                                                                                  2451
                                           2331
                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 75
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: 5.25 in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Godowski.
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                             778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Dreger, Ginger R. REGISTRATION NUMBER: 33,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: UFILING DATE: 19920518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                   aaggtggaggaggaaggaagccccggggaccccgaccacgaggccagcacccagggtcgg 1017
                                                                                                 caagacaagctgcggaggttcaagcccagctctctgccgcatccgctcgagggctccagg
                                                                                                                                                                                                                  cagctggtgcacttcgcctgggagcacttccggccccgctgcaagttcgtctgggggccc
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: NUCLEIC ACID
NDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       i, Paul J. Lokker, Nathalie A. Mark, Melanie R SINGLE-CHAIN HEPATOCYTE GROWTH FACTOR VARIANTS
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                                                                                                                                                                                                                                                                                                                                                                                             Score 57.2; DB 1;
Pred. No. 0.0013;
0; Mismatches 358;
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US-07-885-971-15
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                                                                                                       Query Match
Best Local Similarity 43.7
Matches 272; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15, Application US/07885971 Patent No. 5328837
                                                                                                                                                                                                                                                                     TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/885
FILING DATE: 19920518
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Godows
                                               TELEPHONE: 415/225-3216
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MEDIUM TYPE: 5.25 inch,
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CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                        TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                 NAME: Dreger, Ginger R.
REFERENCE/DOCKET NUMBER: 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                           Score 57.2; DB 1;
Pred. No. 0.0013;
0; Mismatches 358;
                                                                                                                                         Length 10596;
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         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/884811
FILING DATE: 18-MAY-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/885971
FILING DATE: 18-MAY-92
ATTORNEY/AGENT INFORMATION:
NAME: MAISCHANG, DIANE L.
REGISTRATION NUMBER: 35,600
                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1078
                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOCTWARE: Winpatin (Genentech) CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                     STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                         MEDIUM TYPE:
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REFERENCE/DOCKET NUMBER:
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VENTION: HEPATOCYTE GROWTH FACTOR VARIANTS
                                                                                                                                                                                                                                                                                                                                                                  Genentech, Inc
                                                                                                                                                                                                                                                          5 inch, 1.44 Mb floppy
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RESULT 13
US-08-194-088B-15
; Sequence 15, Application US/08194088B
; Patent No. 5580963
; Patent No. 5580963
; APPLICANT: Godowski, Paul J. Lokker, Nathalie A.
; TITLE OF INVENTION: SINGLE-CHAIN HEPATOCYTE GROWTH
; NUMBER OF SEQUENCES: 21
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 10596 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 3.6%;
Best Local Similarity 43.2%;
Matches 272; Conservative
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
STREET: 460 Point San
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TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
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Pred. No. 0.0013;
0; Mismatches 358;
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CITY: SC STATE: C COUNTRY:

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Best Local Similarity 43.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Gallegos, R. Thomas
REGISTRATION NUMBER: 32,692
REFERENCE/DOCKET NUMBER: 755D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-2614
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                1198 ctgagccggcgggagcagccccacagagccaggccctcagagtgcctcagaggtggag
                                                                                                                                                                                                                                                                                                                                                                     2331
                                                                                                        2631
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 07/8:
FILING DATE: 18-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PAtin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/1:
FILING DATE: 09-FEB-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch,
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                                                                                                                                                                                                                                 958 aaggtggaggaaggaagccccggggaccccgaccacgaggccagcacccagggtcgg 1017
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
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acctgtgggccagagcatagcaagggtggggcagggtggacgagggggcccagccacgg
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nucleic acid
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09-FEB-1994
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US-08-194-087-15
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Best Local Similarity
Matches 272; Conserv
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
    2451
                                                                2391
                                                                                                                                                                                2271 CAGGAGCAGGAGGGGCAGGAGCAGGAGGGGGCAGGAGGGGGAGGGGCAGGAG 2330
                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Godowski, Paul J. Lokker, Nathalie A. Mark, Melanie R. TITLE OF INVENTION: HEPATOCYTE GROWTH FACTOR PROTEASE DOMAIN VARIANTS
                                                                                                                                                                                                       LENGTH: 10596 bases
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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CITY: South San Francisco
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SYSTEM: PC-DOS/MS-DOS
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18-MAY-1992
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3ER: 779
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Pred. No. 0.0013;
0; Mismatches 358;
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RESULT 15
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PCT-US93-04648-15
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APPLICANT: Genentech, Inc., Godows
                                            TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10596 bases
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                          APPLICATION NUMBER: 07/884811
FILING DATE: 18-MAY-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/885971
FILING DATE: 18-MAY-92
ATTORNEY/AGENT INFORMATION:
                                                                                                                                         NAME: Dreger, Ginger R.
REGIZION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 75:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
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MEDIUM TYPE: 5.25 inch,
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CORRESPONDENCE ADDRESS:
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                                                                                            TELEFAX: 413/771-7168
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CITY: South San Francisco
STATE: California
                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PRILING DATE: 19930517
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               TOPOLOGY:
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             linear
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Similarity 43.2%;
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Search completed: October 12, 2000, 17:20:35 Job time: 28799 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
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US-07-884-811-15
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US-08-946-026-23
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Sequence 17, Appli
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: APPLICANT: NUSSENZWEIG, VICTOR
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5171843-10
Patent No. 5171843
APPLICANT: NUSSENZWEIG, VICTOR
ITTLE OF INVENTION: IMMUNOGENIC POLYPEPTIDE AND
PURIFYING IT
NUMBER OF SEQUENCES: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.3%; Score 73.8; DB 7; Best Local Similarity 58.4%; Pred. No. 1.1e-08; Matches 129; Conservative 0; Mismatches 92;
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APPLICATION NUMBER: US/07/175,112
FILING DATE: 30-MAR-198
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 754,645
FILING DATE: 9-JUL-1985
APPLICATION NUMBER: 115,634
FILING DATE: 26-OCT-1987
APPLICATION NUMBER: 649,903
FILING DATE: 12-SEP-1984
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APPLICATION NUMBER: 754,645
FILING DATE: 9-JUL-1985
APPLICATION NUMBER: 115,634
FILING DATE: 26-OCT-1987
APPLICATION NUMBER: 649,903
FILING DATE: 12-SEP-1984
SEQ ID NO:8:
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PATCHI NO. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TITLE ; PURIFYING
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Best Local S
Matches 129
                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATENTIAL PC-DOS/MS-DOS
SOFTWARE: PATENTIAN Release #1.0, V
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/232,463
APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY_AGENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: [
FILING DATE:
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FILING DATE: 30-MAR-1988
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                           STREET: 1800 Dia
CITY: Alexandria
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ZIP: 22313-0299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      y Match 3.3%;
Local Similarity 58.4%;
hes 129; Conservative
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Pred. No. 1.4e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                          Suite 500
                                                                                                                                                                                            Version
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1.4e-08;
hes 92;
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; CLONE: pTZgpt-F1s
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                          US-08-993-228-9
                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application Patent No. 5976838
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
                                                                                                              APPLICANT: LAVALIE, Edward R.
APPLICANT: Racie, Lisa A.
APPLICANT: Merberg, David
APPLICANT: Traccy, Maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Vikki
APPLICANT: Agostino, Michael J.
APPLICANT: ESCRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1768 gggccagagcaagctgcctctaagagc 1794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1408 agggtggctaatgaggtaagaaagcggaggaaggtggaggaaggggctgagggtgatgga 1467
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pair
                                                 STREET: 87 Cambr
CITY: Cambridge
STATE: MA
                                                                                                                                                                                                                                                                                                 APPLICANT: Jacobs, Kenneth APPLICANT: McCoy, John M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 3.3%; Score 73.8; DB 1; Length 7218;
Local Similarity 3.9%; Pred. No. 3.1e-08;
nes 15; Conservative 235; Mismatches 137; Indels 0
                    COUNTRY: UZIP: 02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                    ADDRESSEE: Genetics Institute, STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RRRRATCGCAAGCTCCCTCGACCTGC 1045
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                                   U.S.A.
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GENERAL INFORMATION:

APPLICANT: Horlick, Robert A.

APPLICANT: Horlick, Robert A.

APPLICANT: Robbins, Alan K.

APPLICANT: Robbins, Alan K.

TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Gen

TITLE OF INVENTION: From multiple Transfected Episomes

FILE REFERENCE: 0867/1D903US1

CURRENT APPLICATION NUMBER: US/09/130,114

CURRENT FILING DATE: 1998-08-06

NUMBER OF SEQ ID NOS: 36

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                   ; SEQ ID NO 2
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: EBNA
US-09-130-114-2
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; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-993-228-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-130-114-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 41,323
TELECOMMUNICATION NUMBER: 41,323
TELEPHONE: (617) 498-8284
TELEPHONE: (617) 876-5851
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4582 base pairs
TYPER: 10161-6014
                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 264; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09130114
Patent No. 5976807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.1%;
Best Local Similarity 80.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
1317 ggtagagaaaattgcccttaaccttgaggagtgtgcccttagccctatcagccaggagcc 1376
                                                                                                                                                            1197 ggatgggaaccagagggatgaagctaagtccctgagtcccaaggagagagcaagaaaaggaa 1256
                                                                                   1257 gttggaggggaacaggcaggagcaggtcccagggggaggcagatccccaggggtgtctctctga 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4431 GCACTAATCTGTTTGTGAGGGAATATCCATTCCCTCACTCTACTCTCCTCACTATC 4486
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                                                          776
                                                                                                                                     59 gcacacatctgtcagtgagggaatgtcaggtctctcactctcctctcctcactatc 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/993,228
                                                        GGACGGGGAGGACGAGGACGGGGAGGACGACGAGGACGAGGACGAGGACGAGGA 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93;
                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                   3.0%;
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                                                                                                                                                                                                                 Score 68; DB 4; Length 1931; Pred. No. 4.1e-07; O; Mismatches 305; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 69.6; DB 4;
Pred. No. 2.5e-07;
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Length

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RESULT 7
US-09-050-863-2
Sequence 2, Application US/09050863
Patent No. 6114111
GENERAL INFORMATION:
APPLICANT: Lao, Ying
APPLICANT: Hang, Betty
APPLICANT: Payan, Don
TITLE OF INVENTION: Mammalian Protein Interaction Cloning
TITLE OF INVENTION: System
TITLE OF SEQUENCES: 5
; MOLECULE T
US-09-050-863-2
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                                                                                ATTORNEY/AGENT INFORMATION:

NAME: S11va, Robin M.

REGISTRATION NUMBER: 38,304

REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEPAX: (415) 949-8711

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        719
                               TOPOLOGY:
                                           STRANDEDNESS:
                                                                                                                                                                                                               APPLICATION NUMBER: US/09/050,863 FILING DATE: 30-MAR-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 94111-4187
                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGAGGACGGGAGGACGAGGACGAGG
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                TYPE:
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                                                                      2580 base pairs
                                            unknown
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US-09-130-114-1/c
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                                                                                                                                                                                                                                                                                                                                                  ; SOFTWARE: FastSEQ 1
SEQ ID NO 1
; LENGTH: 5452
; TYPE: DNA
; ORGANISM: VEBNA
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 136; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application Patent No. 5976807
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Horlick, Robert A.
APPLICANT: Damaj, Bassam B.
APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
TITLE OF INVENTION: From Multiple Transfected Episomes
FILE REFERENCE: 0867/1093US1
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ
                                                                                                                                    1639
                                                                                                                                                                                          1579
  1826
                      1759 caggtggtggggccagagcaag 1780
                                                                                                                                                                                                                                1519 gagtgtcctgaggcccaaaaggatgggaatgggccagaggactcaaaacagccaggttggg 1578
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les 136; Conserv
                                                                      aacagccaggtcgggccagaggacccaaacagccaggtcgggccagaggacccaaacagc 1758
                                                                                                                            gacccaaacagccaggtcgggccagaggacccaaacagccaggtcgggccagaggaccca 1698
                                                                                                                                                                             gcagaggattccaaaagccaggtggggccggaggatccaaacagccaggtggggctggag 1638
GAGGAGGGCAGGAGCAGGAGG 1805
                                                                                                                                                            aacagccaggtcgggccagaggacccaaacagccaggtcgggccagagggacccaaacagc 1758
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Pred. No. 2.9e-05;
0; Mismatches 126;
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RESULT 9 US-07-884-811-15

Sequence 15, Application US/07884811 Patent No. 5316921

GENERAL INFORMATION:

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RESULT 10
US-07-885-971-15
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Best Local Similarity
Matches 136; Conserv
Sequence 15, Application US/07885971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 75:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
                                                                                                                                                                                                                                                                                         1579 gcagaggattccaaaagccaggtggggccggaggatccaaacagccaggtggggctggag 1638
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: patin (Genentech) CURRENT APPLICATION DATA:
                                                                                                        1759 caggtggtggggccagagcaag 1780
                                                                                                                                                                1699 aacagccaggtcgggccagaggacccaaacagccaggtcgggccagaggacccaaacagc 1758
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: GODOWSKI, Paul J. Lokker, Nathalie A. Mark, Melanie R. TITLE OF INVENTION: SINGLE-CHAIN HEPATOCYTE GROWTH FACTOR VARIANTS NUMBER OF SEQUENCES: 21
                                                                               2559 GAGGAGGGCAGGAGCAGGAGG
                                                                                                                                           TYPE: NUCLEIC ACID
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TELEX: 910/371-7168
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CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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Pred. No. 5.3e-05;
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RESULT 11
US-08-087-783A-15
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10596 harmore
Sequence 15, Application US/08087783A
Patent No. 5547856
GENERAL INFORMATION:
APPLICANT: GODOWSK1, Paul J., Lok:
TITLE OF INVENTION: HEPATOCYTE GR
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Best Local Similarity 51.9%;
Matches 136; Conservative
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APPLICANT: Godowsk1,
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/885,97
FILING DATE: 19920518
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy
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                                                                                                                                                                                                     1759 caggtggtggggccagagcaag 1780
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                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 10596 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 77
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ZIP: 940
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linear
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HEPATOCYTE GROWTH FACTOR PROTEASE DOMAIN VARIANTS
 Paul J., Lokker, Nathalie A., Mark, HEPATOCYTE GROWTH FACTOR VARIANTS
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Pred. No. 5.3e-05;
0; Mismatches 126;
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RESULT 12
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REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: 90755779P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-4416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SED ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1059 base pairs
                 Sequence 15, Application US/08194088B Patent No. 5580963
GENERAL INFORMATION:
APPLICANT: GOGOWSKI, Paul J. Lok
TITLE OF INVENTION: SINGLE-CHAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: 07/884
FILING DATE: 18-MAY-92
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 07/885
FILING DATE: 18-MAY-92
ATTORNEY/AGENT INFORMATION:
NAME: MATSCHAFT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1519 gagtgtcctgaggcccaaaaggatgggaatgggccagaggactcaaacagccaggttggg 1578
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   NUMBER OF SEQUENCES:
                                                                                                                                                                        2559 GAGGAGGGCAGGAGCAGGAGG 2580
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
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ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 51.9
nes 136; Conservative
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FILING DATE: 13-Jul-1993
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Nucleic Acid
DEDNESS: Single
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51.9%;
, Paul J. Lokker, Nathalie A. SINGLE-CHAIN HEPATOCYTE GROWTH 21
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Pred. No. 5.3e-05;
0; Mismatches 126;
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                Mark, Melanie
FACTOR VARIANT
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RESULT 13
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                                                                               Sequence 15, Application US/08194087
Patent No. 5879910
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J. Lo
TITLE OF INVENTION: HEPATOCYTE G
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Best Local Similarity
Matches 136; Conserv
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
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FILING DATE: 09-FEB-1S
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0;
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
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LENGTH: 10596 bases
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,088B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 32,692
REFERENCE/DOCKET NUMBER: 755
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-2614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 18-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gallegos, R. Thomas
REGISTRATION NUMBER: 32,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 415/2-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
TOPOLOGY: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                               gacccaaacagccaggtcgggccagaggacccaaacagccaggtcgggccagaggaccca 1698
                                                                                                                                                                                                                                    GAGGAGGGCAGGAGGAGG 2580
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Pred. No. 5.3e-05;
0; Mismatches 126;
                                                                               Lokker,
TE GROWTH
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                                                                                 Nathalie A. Mark, FACTOR PROTEASE DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 10596;
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10596 bases
                                                                                                                                                                       Sequence 15, Application PC/TUS9304648 GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Godows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.7%;
Best Local Similarity 51.9%;
Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,01
FILING DATE: 18-MAY-1992
COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1579 gcagaggattccaaaagccaggtggggccggaggatccaaacagccaggtggggctggag 1638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                           TITLE OF INVENTION: HEPATOCYTE NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                       2559 GAGGAGGGCAGGAGCAGGAGG 2580
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                             ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 77'
                                 COUNTRY: UZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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360 Kb floppy disk
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Pred. No. 5.3e-05;
0; Mismatches 126;
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 COMPUTER READABLE FORM
                COUNTRY: U
ZIP: 22042
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US-09-010-928B-3
; Sequence 3, Application US/09010928B
; Patent No. 5994099
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                                                                                                    GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V
APPLICANT: Hayashi, Cheryl Y
TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND
TITLE OF INVENTION: CODING THEREFOR
NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART,
STREET: 8110 GATEHOUSE RD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04
                                                                                                                                                                                                                                                                                                                                                                                                                                   1759 caggtggtggggccagagcaag 1780
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/88
FILING DATE: 18-MAY-92
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                2559 GAGGAGGGCAGGAGCAGGAGG 2580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 75
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEPEAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
STREET: 8110 GATEHO
CITY: FALLS CHURCH
STATE: VIRGINIA
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TYPE: NUCLEIC ACID
TYPE: Sing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07
FILING DATE: 18-MAY-92
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                                                  KOLASCH &
SUITE 500E
                                                                     & BIRCH
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,928B
FILING DATE: 22-7AN-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28977
REFERENCE/DOCKET NUMBER: 1447-109P
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2824 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: -
Search completed: October 14, 2000, 03:54:22 Job time: 4774 sec
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LOCATION:
1.2824
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
                                                                                                                                                            1791 gagccctgtggagga 1805
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                                                                                                                      1258 GGACCTGGAGGTGAA 1272
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                                                                                                                                                                                                                                                                                                                                                                                                                      1078 GGAGGTGAAGGACCCGGTGGTGGTGGTGGTGGTGGTGGACCT 1137
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taken from 3' region. Stop codon begins at position 2722."
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Minimum DB seq length: Maximum DB seq length:
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Perfect score:
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                                                                                                                                                       Score
   length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                        | SIDSI/gcgdata/geneseq/geneseqn/Na1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn/Na1981.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn/Na1981.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn/Na1982.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn/Na1983.DAT:*
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Gapop 10.0 , Gapext 1.0
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2250
1 tgggctcagccacg
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Copyright (c) 1993 - 2000 Comp
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8 N71064
19 V46316
20 X40045
21 Z33356
19 V22704
21 A08554
19 V55831
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X90923
X33181
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5716.496 Million cell updates/sec
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Gene encoding Plas
Human secreted pro
Prostate cancer as
Human secreted pro
Mouse recombinase
Murine REC2 serine
Nucleotide sequenc
Epstein Barr Virus
Anti-sense strand
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375	5668	3848	2323	1378	941	3121	2608	2773	921	1707	1534	863	791	497	4673	2639	2171	1711	2042	756	1835	746	1037	722	10596	10596	10596	10380	9600	8705	7996	7797
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T84939	X27262	X27277	V59524	V59706	N30062	Z94131	A26286	Z65009	Z65349	Z52500	Z20856	T91302	X19493	A37132	Q27189	A37137	V73006	V43617	Z41321	A02602	X27245	X86455	A26447	X06786	X15650	T40348	Q51731	Z22248	V21683	Z23778	3318	X33180
Human prostate pro	Prostate-tumour de	a	Human secreted pro	Human secreted pro	Sequence of a modi		Human secreted pro		Human secreted pro	Human secreted pro	Polynucleotide seq	Human H1075-1 secr	Human secreted pro	an PRO1561	N	PRO1788 (ñ		norma	-	CLARI	encoding	secre	dult	ide	Plasmid pCisEBON f	Plasmid pciseBON f	ide	ש	Vector pShuttle DN	equence of	Cowpox virus bsr f

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ALIGNMENTS

misc_feature CDS 06-MAY-1993 (first entry) repeat_unit repeat_unit repeat_unit Plasmodium vivax. Malaria; vaccine; immunogenic polypeptide; ss Plasmodium vivax circumsporozoite (CS) gene. repeat_unit repeat_unit /*tag= f /note= "encodes i 400..426 /*tag= e /note= "encodes 373..399 /*tag= c /note= "encodes 319..345 /*tag= a
/note= "circumsporozoite protein"
247..945 /*tag= d /note= "encodes 346..372 /note- "DNA 292..318 Location/Qualifiers *tag= fragment encoding immunogenic polypeptide" immunogenic repetitive sequence immunogenic repetitive sequence immunogenic repetitive sequence " immunogenic repetitive sequence

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12-SEP-1984;
09-JUL-1985;
26-OCT-1987;
30-MAR-1988;
  The sequence gene, the CS
                                        New recombinant produced immunogenic poly:peptide -part of P. vivax circumsporozoite protein and anothe conserved among different species
                          Disclosure; Page 14;
                                                                                                  Nussenzweig V;
                                                                            P-PSDB;
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697..723
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724..750
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Best Local S
Matches 129
The circumsporozoite protein of P. vivax sporozoites this gene is useful in the construction of an anti-ma
                                                                                                            New Plasmodium vivax circumsporozoite protein - peptide(s) contg. its dominant epitope, useful vaccines
                                                                                                                                                                                                    WPI; 1987-037250/05
P-PSDB; P70708.
                                                              Disclosure; fig. 3; 32pp; English
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                                                                                                                                                                                                                                                                       Arnot DE,
                                                                                                                                                                                                                                                                                                                                                                                  12-JUL-1985;
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       New isolated nucleic acids and secreted proteins - isola human foetal kidney, adult placenta, adult colon, adult foetal brain and adult brain cDNA libraries
                                                                                                                                                                                                                                                                                                                differentiation;
                                                                                                                                                                                                                                                                                                                                                               16-OCT-1998
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                                                                                   Agostino
                                                                                                                         18-DEC-1997;
10-JAN-1997;
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                                                                                                                                                                                                                                                                                           haemostatic;
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DB; W64468.
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97US-0781225
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/note= "isolated from clong
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Treacy M;
                                                                                                                                                                                                                                                                                          receptor; ligand; anti-inflammatory;
                                                                                                                                                                                                                                                                                                   n; cytokine; cell proliferation; activin;
stem; stimulator; suppressor; tissue growth;
inhibin; chemotactic; chemokinetic; cadherin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 73.8; DI
Pred. No. 7.9e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                           from clone CW420_2.
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No. 7.9e-07;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence encodes a novel secreted protein from clone CW420_2 isolated from a human fetal brain cDNA library. This novel protein may have biological activity, e.g. nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity or other activities.
                                                                                                                                                                                                                                                                                                                                                                               22-JUN-1998;
17-JUL-1997;
10-OCT-1997;
10-OCT-1997;
10-OCT-1997;
11-OCT-1997;
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                                                                 Claim 67; Page 646; 787pp; English
                                                                                                             New isolated cancer associated nucleic acids and polypeptides isolated using sera from cancer patients, used to develop proof or the diagnosis, monitoring or treatment of cancers
                                                                                                                                                                                                                                                                   Chen Y, Gout
Pfreundschuh 1
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97US-0896164.
97US-0061599.
97US-0061765.
97US-0948705.
97GB-0021697.
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Scanlan MJ,
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Pred. No. 8.1e-06;
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cancer; renal cancer;
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The invention relates to by expression of a human

a method for diagnosing a cancer associated antigen

disorder characterised precursor coded for by

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Best Local Similarity
Matches 165; Conserv
07-MAY-1998;
02-JUN-1998;
22-JUL-1998;
31-JUL-1998;
10-AUG-1998;
11-AUG-1998;
06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                  07-MAY-1999;
                                                                                                                                          11-NOV-1999
                                                                                                                                                                                                                             haematopoiesis regulation;
chemotactic; chemokinetic;
ligand; anti-inflammatory;
tumour inhibition; gene the
                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                         WO9957132-A1
                                                                                                                                                                                                                                                                                        differentiation;
                                                                                                                                                                                                                                                                                                                              Human secreted protein clone fm3_1 nucleotide sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                           29-FEB-2000 (first entry)
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                                                                                                                                                                                                                                                                                  secreted protein; nutritional; cytokine; cell proliferation; entiation; immune stimulating; vaccine; suppression;
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98US-0084564.
98US-0087645.
98US-0094712.
98US-0094935.
98US-0095880.
98US-0096068.
99US-0096068.
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tissue growth; activin; inhibin;
haemostatic; thrombolytic; receptor;
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No. 7.7e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes new human secreted proteins which were considered from adult placenta, adult retina, foetal brain, foetal kidney, adult blood, adult blood, adult brain, adult trestal, adult blood, adult blooder, adult neural consistency adult testes, and adult lymph node cDNA ilbraries. The human conserved proteins, and the polynucleotides encoding them, are predicted to have biological activities which would make them suitable for containing preventing or ameliorating medical conditions in humans and cannals. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating contivity, as a vaccines) or suppressing activity, haematopoissis regulating contivity, tissue growth activity, activin/inhibin activity, contivity, tissue growth activity, activin/inhibin activity, cativity, receptor/ligand activity, anti-inflammatory activity, cativity, receptor/ligand activity, anti-inflammatory activity, activity, and tumour inhibition contivity. The polynucleotides are also stated to be useful for gene contivity. The polynucleotides are also stated to be useful for gene contivity. The polynucleotides are also stated to be useful for gene continued the polynucleotides are also stated to be useful for gene continued the polynucleotides are also stated to be useful for gene continued the polynucleotides are also stated to be useful for gene continued the polynucleotides are also stated to be useful for gene continued the polynucleotides are also stated to be useful for gene continued the polynucleotides are also stated to be useful for gene continued the polynucleotides are also stated to be useful for gene continued the polynucleotides are also stated to be useful for gene continued the polynucleotides are also stated to be useful for gene continued the polynucleotides are also stated to be useful for gene continued the polynucleotides are also stated to 
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                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                             apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V22704 standard; cDNA; 1525 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2228 ааааааааааааааааааааа 2250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse recombinase muREC2 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 641 BP; 219 A; 146 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 90; Page 436; 492pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides encoding secreted human proteins, adult placenta, adult retina, fetal brain, fetal -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jacobs K, McCoy JM, LaVal
Merberg D, Treacy M, Agos
DiBlasio-Smith E, Widom A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GEMY ) GENETICS INST INC
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                                                                                                                                                                                                                                                                                                                                                                                                             e; REC2; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                  Location/Qualifiers 16..1068
                                                                                                                                                                                                                                                                                                                                                                                                         hsREC2; homologous transgenic animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.7%;
83.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LaVallie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Agostino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 60.6; DB 21 Pred. No. 0.00036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89 G; 187 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Collins-Racie LA,
Steininger RJ,
                                                                                                                                                                                                                                                                                                                                                                                                             recombination; irradiation;
knock-out mouse; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
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Matches 87
                                                                                                                                                                                                                                                                                                                                                                                                      1384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REC2 in a cell was found to facilitate homologous recombination between an exogenous DNA and the genome of a cell. It also sensitises the cell to DNA damage, e.g. by gamma or UV radiation or from cytotoxic agents. This causes the cell to undergo apoptosis in response to DNA damage. MuREC2 can be used to construct transgenic animals. REC2 knock-out mice are useful as models for tumorigenesis induced by chemical carcinogens. The harEC2 human homologue gene (see V22703) is also claimed, which can be used in
                                                                                                                                                                                                                                                                                                                               2240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This polynucleotide corresponds to the mouse homologue, the REC2 gene (UmREC2) of Ustilago maydis, and codes fo dependent recombinase (see W56265). Overexpression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalian and human REC2 genes - useful for the sensitisation
                                                                                                          Mus musculus
                                                                                                                                phosphorylation;
                                                                                                                                                                                             19-JUL-2000
                                                                                                                                                                                                                                            A08554 standard;
                                                                                                                                                                                                                                                                                                       1504 aaaaaaaaaa 1514
                                                                                                                                                                                                                                                                                                                                                                                                                            2120 ccctaagggtctagagggaggggcctcttcattagtctggtgccaagtgaggccttttct 2179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rnıs polynucleotide
the REC2 gene (UmREC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 12; Fig 1G; 88pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; W56265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 66.4
mes 87; Conservative
                                                                                                                                                                                                                                                                                                                     |||||||||||
                                                                                                                                                                                                                                                                                                                                                                   cccctagggagagcaggaggggactaacaagatttgtaattacagaagggaaaatttcc
                                                                                                                                                                                                                                                                                                                                                       REC2
                                                                                                                                serine kinase; homologous pairing; strand transfer; rylation; cyclin E; p53; cell cycle; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1525 BP; 450 A; 330
                                                                                                                                                                   serine kinase encoding sequence.
                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kmiec EB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-0025929.
                                                                     Location/Qualifiers
                                                                                                                                                                                                                                          DNA; 1525
                                             product= Rec2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rice MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 60.6; DB 19;
Pred. No. 0.00048;
0; Mismatches 44;
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of cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Overexpression of mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP-dependent recombinase(s) to the apoptotic effects of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ή,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1525;
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Matches 87
rusion protein; stabilising polypeptide; proteolytic degradation; resistance; half-life; autoimmune disease; inflammation; nitro drug; IkappaB regulator protein; inflammatory bowel disease; in vivo imaging; nitroreductase protein; enzyme therapy; prodrug therapy; protease; cancer; pathological condition; ss.
                                                                                                                                                                                                                                                                                                  1504
                                                                                                                                                                                                                                                                                                                                                                    1444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in the same supergene family as the mammmalian protein having homologous pairing and strand transfer activities, RAD51 and was isolated because of its homology to the homologous pairing and strand transfer protein of Ustilago maydis. In particular, muRec2 phosphorylates several proteins that control the cell cycle, especially cyclin E and p53. The invention permits the phosphorylation of cell cycle control proteins at sites that are physiologically relevant. The invention can be practiced with either murine or human Rec2 or a mutein or chimera of these proteins. In particular the mutein has the sequence of a Rec2 kinase containing other than a Tyr at position 163. The invention comprises a method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2120 ccctaagggtctagagggagggcctcttcattagtctggtgccaagtgaggccttttct 2179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphorylating a serine-containing substrate comprising incubating the substrate with ATP (adenosine triphosphate) and Rec2 kinase or a mammalian Rec2 and measuring the level of phosphorylation. The method is useful for discovering compounds which are specific antagonists or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphorylating a serine-containing substrate by incubating it with adenosine triphosphate and Rec2 kinase and measuring the level of phosphorylation, useful for discovering specific antagonists or
                                                                                                                                                                                                            V55831 standard; DNA; 799
                                                                                                                                                                                                                                                                                                                  2240 aaaaaaaaaaa 2250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful for discovering agonists of Rec2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phosphorylation,
agonists of Rec2
                                                                                                             Nucleotide
                                                                                                                                            18-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1525 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYJE-) UNIV JEFFERSON THOMAS (CORR) CORNELL RES FOUND INC (KIME-) KIMERAGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                  aaaaaaaaa 1514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87; Conservative
                                                                                                         sequence of the stabilising sequence-encoding insert.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence encodes the muRec2, a murine serine kinase.
                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         450 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Holloman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 60.6; DB 21;
Pred. No. 0.00048;
0; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         370 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kmiec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         375 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is a nucleotide sequence of the stabilising sequence-encoding CC insert. The invention provides a method for increasing the resistance of a core protein to proteolytic degradation that comprises linking or CC inserting onto or into the core protein a stabilising polypeptide of CC formula [(Glya)X(Glyb)Y(Glyc)2]n where Glya, Glyb, Glyc are 1-6 cc sequential Gly residues and X, X, Z are Ala, Ser, Val, IIe, Leu, Met, Phe, Pro or Thr and n can be anything between 1-66. X, Y and Z need not CC be identical from n repeat to n repeat. Alternatively a nucleic acid encoding the stabilising polypeptide can be linked onto or inserted into a nucleic acid encoding a core protein. The fusion proteins of the livention are more resistant to degradation by proteases and, thus, have CC invention are more resistant to degradation by proteases and, thus, have compare half-life than the unfused core protein. The products can be cused for treating autoimmune diseases, cancer and inflammation. In particular, the core protein may be an IxappaB regulator protein for the CC treatment of inflammatory bowel disease, or a nitroreductase protein conditions. The fusion proteins can also be used in or other pathological conditions. The fusion proteins can also be used in CC disangustic methods such as in vivo immedian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnostic methods such as in vivo imaging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New fusion proteins resistant to proteolytic degradation comprising a core protein with a stabilising polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 4B; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a peptide sequence containing glycine repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-312463/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JUN-1997;
15-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Epstein-barr virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
mes 136; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                 gagtgtcctgaggcccaaaaggatgggaatgggccagaggactcaaacagccaggttggg 1578
                                                                         gaggaggggcaggagcaggagg 375
                                                                                                          caggtggtggggccagagcaag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP;
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96US-0030986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 A; 106 C; 479 G; 13 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 60.4; DB 19
Pred. No. 0.00043;
); Mismatches 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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Qy Б β

356

1579 gcagaggattccaaaagccaggtggggccggaggatccaaacagccaggtggggctggag 1638

gagtgtcctgaggcccaaaaggatgggaatgggccagaggactcaaacagccaggttggg 1578

Best Local Similarity 51.9 Matches 136; Conservative

51.9%;

Score 60.4; DB 20 Pred. No. 0.00056; 0; Mismatches 126

20;

Indels

0;

Gaps

0

0;

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Antigen I (EBNA 1), which is obtained from commercially available plasmid proverse. But it is not to be stably maintain episomes containing EBV origin of replication (orif) and a gene encoding protein or RNA of interest. Eucaryotic host cells expressing EBNA 1 protein are transfected with these episomes to produce recombinant cell lines expressing multiple genes of interest. This provides a rapid and reliable method of stably expressing multiple genes in transfected cells. The episomes are useful in the transfection of genes encoding receptors, transporter proteins, ion channels, adhesion molecules and transcription factors. The episomes carrying desired genes can also be used to transfect cells in gene therapy, antisense therapy, for gene amplification, cell immortalisation, etc.
Sequence 1925 BP; 486 A; 352 C; 872 G;
                                                                                                                                                                                                              The present sequence is a DNA encoding Epstein Barr Virus Nuclear Antigen 1 (EBNA 1), which is obtained from commercially available
                                                                                                                                                                                                                                                                                                 New method useful for
                                                                                                                                                                                                                                                                                                                                                                                                   Damaj
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-MAR-1998;
06-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            multiple gene expression; transporter protein; transcription factor; adhesion molecule; antisense therapy; gene amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Epstein Barr Virus Nuclear Antigen 1 DNA; plasmid pCMVEBNA; EBN episome; transfection; origin of replication; EBV orip; receptce eucaryotic host cell; recombinant cell line; ion channel; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                (PHAR-) PHARMACOPEIA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-SEP-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X90924 standard; DNA; 1925 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Epstein-barr virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immortalisation;
                                                                                                                                                                                                                                                                                                                                                                                                 BB,
                                                                                                                                                                                                                                                                24; Fig 2; 86pp; English.
                                                                                                                                                                                                                                                                                                                for expressing genes from recombinant eukaryotic cells,
                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                 Horlick RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virus Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0040961
98US-0130114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US03307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "EBNA 1"
/trans1_except= (pos:799..800, aa:Gly)
/note= "The sequence is described throughout the specification as being 1926 nucleotides long, but sequence of only 1925 bp has been given in figure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antigen 1 (EBNA 1)
215 T; 0 other;
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oriP; receptor;
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       The present sequence is an anti-sense strand of commercially available plasmid pCMYDBNA from which Epstein Barr Virus Nuclear Antigen 1 (EBNA 1) encoding DNA is obtained. EBNA 1 protein is used to stably maintain episomes containing EBV origin of replication (orif) and a gene encoding protein or RNA of interest. Eucaryotic host cells expressing EBNA 1 protein are transfected with these episomes to produce recombinant cell lines expressing multiple genes of interest. This provides a rapid and reliable method of stably expressing multiple genes in transfected cells. The episomes are useful in the transfection of genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-sense strand; plasmid pCMVEBNA; EBNA 1; episome; transfection; Epstein Barr Virus Nuclear Antigen 1; origin of replication; EBV orip; eucaryotic host cell; recombinant cell line; ion channel;
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                                                                                                                              Example
                                                                                                                                                                  New method
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06-AUG-1998;
                                                                                                                                                                                                                                                                                                 12-FEB-1999;
                                                                                                                                                                                                                                                                                                                         23-SEP-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Epstein-barr virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    multiple gene expression; receptor; transporter protein; ge
transcription factor; adhesion molecule; antisense therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-sense
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1759 caggtggtggggccagagcaag 1780
                                                                                                                                                                                                                                    (PHAR-) PHARMACOPEIA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          596
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                                                                                                                                                     for
                                                                                                                            1; Fig 1; 86pp;
                                                                                                                                                                                                              Horlick RA,
                                                                                                                                                    gene therapy
                                                                                                                                                               for expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           strand
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                                                                                                                                                                                                                                                             98US-0040961.
98US-0130114.
                                                                                                                                                                                                                                                                                                 99WO-US03307
                                                                                                                                                                                                                                                                                                                                                                   /product= "EBNA 1 protein"
/note= "Epstein barn"
                                                                                                                                                                                                                                                                                                                                                                                                      complement (3032..4957)
                                                                                                                                                                                                                                                                                                                                                                                                                   location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           얁
transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell immortalisation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pCMVEBNA plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5452
                                                                                                                              English.
                                                                                                                                                                                                               Robbins
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proteins,
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                                                                                                                                                                  from
                                                                                                                                                                                                                                                                                                                                                                     Virus Nuclear
                                                                                                                                                                recombinant eukaryotic cells,
 not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
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                                                                                                                                                                                                                                                                                                                                                                                         1826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    can
for
                                                                                                                                                                                                                                                             Cowpox virus; bsr; viral vector; expression; a crmA; bcl-2; bcl-x1; FLIP; survivin; IAP; ILP;
                                                                                                                                                                                                                                                                                                                                                                                                          1759
                                                                                                                                                                                                                                                                                                                                                                                                                            1886
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                                                                                                                                                             07-SEP-1998;
                                                                                                                                                                                                                                                    autoimmune disease; graft rejection
                                                                                                                                                                                                                                                                                        Base sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1519 gagtgtcctgaggcccaaaaggatgggaatgggccagaggactcaaacagccaggttggg 1578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   molecules and transcription factors. The episomes carrying desired genes can also be used to transfect cells in gene therapy, antisense therapy, for gene amplification, cell immortalisation, etc.
                                                    Example 1;
                                                                                      WPI; 1999-243728/20
                                                                                                         Hamada
                                                                                                                                          08-SEP-1997;
                                                                                                                                                                               18-MAR-1999.
                                                                                                                                                                                                 WO9913073-A2
                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                            X33181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                         (RPRG-) RPR
                                                                                                                                                                                                                 Cowpox virus.
                                                                                                                                                                                                                                           inflammatory disease; ss.
                                                                                                                                                                                                                                                                                                          25-JUN-1999
                                                                                                                                                                                                                                                                                                                                            X33181 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local 136;
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                                                                     apoptosis-resistant virus-sensitive
                                                                                                                                                                                                                                                                                                                                                                                         GAGGAGGGGCAGGAGCAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gcagaggattccaaaagccaggtggggccggaggatccaaaacagccaggtggggctggag 1638
                                                                                                                                                                                                                                                                                                                                                                                                        caggtggtggggccagagcaag
                                                                                                                                                                                                                                                                                                                                                                                                                            aacagccaggtcgggccagaggacccaaacagccaggtcgggccagaggacccaaacagc 1758
                                                                                                                                                                                                                                                                                                                                                                                                                                                               gacccaaacagccaggtcgggccagaggacccaaacagccaggtcgggccagaggaccca 1698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5452
                                                   Page 38-41;
                                                                                                                         GENCELL ASIA PACIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                       of the plasmid pRx-ires-bsr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B₽;
                                                                                                                                           97JP-0259235
                                                                                                                                                             98WO-JP04010
                                                                                                                                                                                                                                                                                                                                            DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.7%;
51.9%;
                                                                                                                                                                                                                                                                                                                                            6644
                                                  51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; 1736 C;
                                                                                                                                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                                                                         1805
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0; Mismatches
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                                                                                                                         INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1246 G;
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                                                                                                                                                                                                                                                    reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126;
                                                                                                                                                                                                                                                                    apoptosis; resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ħ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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The present invention describes an apoptosis-resistant virus-sensitive cell line into which an apoptosis resistance gene has been introduced. The recombinant viruses generated are capable of expressing apoptosis-associated genes. These can then be used in a variety of diseases for which the induction of apoptosis by gene transfer, or where the

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RESULT 12
X33182
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Best Local S
Matches 79
The present invention describes an apoptosis-resistant virus-sensitive cell line into which an apoptosis resistance gene has been introduced. The recombinant viruses generated are capable of expressing apoptosis-associated genes. These can then be used in a variety of diseases for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cowpox virus; bsr; viral vector; expression; apoptosis; resistance; crmA; bcl-2; bcl-x1; FLIP; survivin; IAP; ILP; adenovirus; cancer; autoimmune disease; graft rejection reaction; inflammation; inflammatory disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example
                                                                                                                                                                                   New apoptosis-resistant virus-sensitive
                                                                                                                                                                                                                                          WPI; 1999-243728/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Base sequence
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                                                                                                                                                                                                                                                                                                                                                (RPRG-) RPR
                                                                                                                                                                                                                                                                                                                                                                                                     08-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ggcctcttcattagtctggtgccaagtgaggccttttctgaataaactctttagactttg 2200
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                                                                                                                               Page
                                                                                                                                                                                                                                                                                                                                                GENCELL ASIA PACIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the plasmid pRx-Bcl-xl-bsr.
                                                                                                                                                                                                                                                                                                                                                                                                     97JP-0259235
                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-JP04010
                                                                                                                                 41-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2166 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7372 BP
                                                                                                                               51pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1573 C; 1424 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 60.4; D pred. No. 0.00 0; Mismatches
                                                                                                                                 English
                                                                                                                                                                                      cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1481 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 6644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            induction
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밁 Ş 밁 Ş

The present invention describes an apoptosis-resistant virus-sensitive cell line into which an apoptosis resistance gene has been introduced. The recombinant viruses generated are capable of expressing apoptosis-associated genes. These can then be used in a variety of diseases for

New

<u>بر</u> Page

34-38;

51pp;

English

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RESULT 13
X33180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cc which the induction of apoptosis by gene transfer, or where the cinhibition of harmful apoptosis, is therapeutic. The recombinant viruses care useful as vectors for gene therapy which can be applied to cancer ct therapy for destroying cancer cells selectively, the treatment of cautoimmune diseases and graft rejection reaction, and apoptosis induction ct therapy for inflammatory cells in inflammatory diseases. Prior arts have encountered the problem where if an adenovirus vector capable of cexpressing an apoptosis associated gene is introduced into animal cells, the cells producing the virus will be destroyed because the period of time required to induce cell death by apoptosis is shorter than that crequired to replicate and produce the virus, resulting in failure to obtain a recombinant virus having the integrated apoptosis-associated gene. In this invention an apoptosis-resistant 293 cell line (having an apoptosis resistant gene introduced) is established and overcomes the prosent sequence represents the base sequence of the cplasmid pRx-Bcl-xl-bsr, which contains the human Bcl-xl gene, and cc is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query
Best I
                                                                                                                                                                                                                                                                                                                                                                    Cowpox virus; bsr; crmA; bcl-2; bcl-x1 autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4466
                                                                                                                                                        Hamada
                                                                                                                                                                                                                                                                                                                            Cowpox virus
                                                                                                                                                                                                                                                                                                                                                                                                                            Cowpox virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2141 ggcctcttcattagtctggtgccaagtgaggccttttctgaataaactctttagactttg
                                                                                                                          WPI; 1999-243728/20
                                                                                                                                                                                 (RPRG-) RPR
                                                                                                                                                                                                              08-SEP-1997;
                                                                                                                                                                                                                                         07-SEP-1998;
                                                                                                                                                                                                                                                                     18-MAR-1999.
                                                                                                                                                                                                                                                                                                 W09913073-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X33180 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7372
                                                                                                                                                                                                                                                                                                                                                      inflammatory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                              apoptosis-resistant virus-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gtcctccgattgactgagtcgcccgggtacccgtgtatccaataaaccctcttgcagttg 4465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79; Conserv
                                                                                                                                                                                    GENCELL ASIA PACIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                    bcl-x1;
                                                                                                                                                                                                                                                                                                                                                                                                                         bsr full length gene sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₿₽;
                                                                                                                                                                                                                                                                                                                                                                                             bsr; viral vector; expression; apoptosis; resistance;
                                                                                                                                                                                                                                         98WO-JP04010
                                                                                                                                                                                                             97JP-0259235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2353 A; 1749
                                                                                                                                                                                                                                                                                                                                                                    ; FLIP; survivin; IAP; ILP;
graft rejection reaction; :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0.00
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 60.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; 1649 G; 1621 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                00085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                     inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2250
                                                                                                                                                                                                                                                                                                                                                                                 cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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RESULT 14
X33184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4891
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The present invention describes an apoptosis-resistant virus-sensitive cell line into which an apoptosis resistance gene has been introduced. The recombinant viruses generated are capable of expressing apoptosis-associated genes. These can then be used in a variety of diseases for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cowpox virus; bsr; viral vector; expression; apoptosis; resistance; crmA; bcl-2; bcl-x1; FLIP; survivin; IAP; ILP; adenovirus; cancer; autoimmune disease; graft rejection reaction; inflammation; inflammatory disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X33184 standard;
                                                                                                                                                                                                                                                                       WPI; 1999-243728/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9913073-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Base sequence of the plasmid pRx-Bcl 2-i-hCD 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                    (RPRG-) RPR GENCELL ASIA PACIFIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                             apoptosis-resistant virus-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gtcctccgattgactgagtcgcccgggtacccgtgtatccaataaaccctcttgcagttg 4890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7797 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.7%;
nilarity 71.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              97JP-0259235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-JP04010
                                                                                                                                                       46-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2542 A; 1760 C; 1656 G;
                                                                                                                                                 51pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 60.4; DB 2
Pred. No. 0.00087
0; Mismatches 3
                                                                                                                                                    English.
                                                                                                                                                                                                             cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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This invention describes a novel method for generating an antisense library targeted to a selected RNA transcript. The methods can be usefor identifying antisense agents and for identifying target sites for

Claim 16;

Page

43-50;

63pp;

English.

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RESULT
Z23778/
ID Z2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           which the induction of apoptosis by gene transfer, or where the inhibition of harmful apoptosis, is therapeutic. The recombinant viruses are useful as vectors for gene therapy which can be applied to cancer therapy for destroying cancer cells selectively, the treatment of autoimmune diseases and graft rejection reaction, and apoptosis induction therapy for inflammatory cells in inflammatory diseases. Prior arts have encountered the problem where if an adenovirus vector capable of expressing an apoptosis-associated gene is introduced into animal cells, the cells producing the virus will be destroyed because the period of time required to induce cell death by apoptosis is shorter than that required to replicate and produce the virus, resulting in failure to obtain a recombinant virus having the integrated apoptosis-associated gene. In this invention an apoptosis-resistant 293 cell line (having an apoptosis resistant gene introduced) is established and overcomes the problem. The present sequence represents the base sequence of the plasmid present sequence represents the base sequence and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18/c
Z23778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2141
                                                                            Production of antisense libraries, used agents and for identifying target sites inhibition of a selected gene
                                                                                                                                                                                                                 28-MAR-1998;
06-NOV-1998;
                                                                                                                                                                                                                                                                                     07-OCT-1999
                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                   Antisense; DNA library; identification; multiple cloning site; inhibition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7996
                                                                                                                                   WPI; 1999-610866/52.
                                                                                                                                                                                        (UTAH ) UNIV
                                                                                                                                                                                                                                                          28-MAR-1999;
                                                                                                                                                                                                                                                                                                               WO9950457-A1
                                                                                                                                                                                                                                                                                                                                                                                                           Vector pShuttle DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ggcctcttcattagtctggtgccaagtgaggccttttctgaataaactctttagactttg 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gtcctccgattgactgagtcgcccgggtacccgtgtatccaataaaccctcttgcagttg 5089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                        UTAH RES FOUND
                                                                                                                                                             Pierce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP;
                                                                                                                                                                                                                 98US-0079792.
98US-0107504.
                                                                                                                                                                                                                                                          99WO-US06742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2463 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.7%;
71.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8705
                                                                                                                                                             Chen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 60.4; DB 20;
Pred. No. 0.00087;
0; Mismatches 31;
                                                                                                                                                             2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1829 G;
                                                                                          for identifying antisense for antisense-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Η,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                 MCS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.7%; Score 60.4; DB 20; Length 8705; Best Local Similarity 51.9%; Pred. No. 0.0009; Matches 136; Conservative 0; Mismatches 126; Indels 0;
                                                                                                                            1699
                                                                                                                                                                                                                                                                                                                                    antisense-mediated inhibition of a selected gene. The use of a direct library for target site selection significantly simplifies the screening process, since only very small libraries need be prepared and assayed. This sequence represents the vector pShuttle which is used in the method of the invention.
7691 GAGGAGGGGCAGGAGCAGGAGG 7670
                            1759 caggtggtggggccagagcaag 1780
                                                                                1639
                                                                                                                                                                                                                                                1579 gcagaggattccaaaagccaggtggggccggaggatccaaaacagccaggtggggctggag 1638
                                                                                                                                                                  Sequence 8705 BP; 1875 A; 2575 C; 2078 G; 2177 T; 0 other;
                                                                                                          aacagccaggtcgggccagaggacccaaacagccaggtcgggccagaggacccaaacagc 1758
                                                                                                                                                                                               gacccaaacagccaggtcgggccagaggacccaaacagccaggtcgggccagaggaccca 1698
                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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Search completed: October 14, 2000, 04:52:20 Job time: 6435 sec

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Minimum DB seq length: Maximum DB seq length:
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RESULT X40044 22-JUN-1998; 17-JUL-1997; 10-OCT-1997; 10-OCT-1997; 10-OCT-1997; 11-OCT-1997; Chen Y, Gout Pfreundschuh Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer; X40044 standard; DNA; 789 Tureci 0; (LUDW-) LUDWIG 28-JAN-1999. WO9904265-A2 Homo sapiens prostate cancer; ss. Prostate cancer associated gene. 02-JUL-1999 X40044; 15-JUL-1998; Gout ĭ (first entry) Į, 98US-0102322. 97US-0896164. 97US-0061599. 97US-0061765. 97US-0948705. 97GB-0021697. INST CANCER RES 98WO-US14679 Gure A, Sahin U, дB O'Hare M, Scanlan MJ, Obata Y, Old , Stockert E; 5

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                                                               Human; secreted protein; expressed sequence tag; EST; haematopoiesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic; receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                   1955
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                                                                                                       EST clone BK517.
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10-APR-1998;
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               15-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                            therapy;
                                                                                                                                                                                                                                                                                                                                                                                                    CCCGGCCCGGCAAGGACTTGCAAGGGACGAAGCCAGCCGAGAAGCCCCATTCGGAAGACCC 644
                                                                                                                                                                                                                                                                                                  TGCTGCGGGCTCCCCTCAGGCTNTGCTTCGTGACCCGTGACCCATGACCCACAGTGCTGG
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nilarity 95.0%;
Conservative
98WO-US06955.
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                                                                                                                       entry)
                                                                                                                                                        375
                                                                                                                                                        ВP
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Pred. No. 6e-89;
3; Mismatches
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Best Local Sin
Matches 301;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1987
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Racie LA,
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Antisense oligonucleotide; multiple target; antisense impaired respiration; inflammation; lung disease;
                                                                                                                      X53491 standard; DNA; 114955
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, Spaulding
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Treacy M;
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Pred. No. 1.9e-44;
2; Mismatches 0;
                                        antisense oligonucleotide
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CC initiation codons, genomic flanking regions, intron-exon borders, the CC initiation codons, genomic flanking regions, intron-exon borders, the CC initiation codons, genomic flanking regions, intron-exon borders, the CC initiation codons, genomic flanking regions, intron-exon borders, the CC or more diseases, conditions or mixtures. The antisense oligonucleotides compared from sequences x55272-74. These multiple target CC oligonucleotides (specifically x55100-271) can be used for the antisense CC treatment of diseases and conditions. Typical diseases and conditions concluding lung diseases, pulmonary vasconstriction, inflammation, CC including lung diseases, pulmonary vasconstriction, inflammation, CC allergic rhinitis, acute asthma, allergies, asthma, impeded respirator, respiratory diseases (COPD), and cancers such as leukemias, lymphomas, CC respiratory disease (COPD), and cancers such as leukemias, lymphomas, CC carcinomas eg. colon cancer, breast cancer, melanoma, hepatic metastases, as well as all types of cancer, melanoma, hepatic contastases, as well as all types of cancers which may metastasize or have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 metastasized to the lungs, including breast and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The specification describes antisense oligonucleotides (X52869-X55271) directed against at least 2 mRNAs selected from target genes, coding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 37; 120pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense oligonucleotides used in
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17-SEP-1997;
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mes 537; Conserv
GAGCCAGGGGCCCNNHNNNSCGGGCCGGGGGCCGAGCCAGGGGCCCNNHNNNSCCGGGC 106345
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                                                                                           HNNNSAGCCGGGCCGCGGGGCCGAGCCAGGGGCCCNNHNNNSAAGCCGGGCCGCGGGGCC
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                                                                                                                                      tgcaagttogtotgggggococeaagacaagotgcggaggttcaagcccaagotototgcoc 936
                                                                                                                                                                                                                       CGCGGGGCCGAGCCAGGGCCCNNHNNNSGCCGGGGCCGGGGCCGAGCCAGGGGCCCNN
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                                                                    GGCGCGCCCNNHNNNSCGGCCCGGCCGGCCGCCCCVNNHNNNSCGGCCCGGCCGGCC
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directed against at least 2 mRNAs selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides may be derived from sequences x55272-74. These multiple target oligonucleotides (specifically x55180-771) can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasoconstriction, inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                               09-JUN-1998;
17-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chronic obstructive pulmonary disease; leukemia; lymphoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic m
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                                                                                                                                                                                                                                                            New antisense oligonucleotides used in treatment of, e.g. pulmonary vasoconstriction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            allergic rhinitis, acute asthma, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, Cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            757
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                         cttgccgggtcccctgccccatcggggcaccccaaggctggacacagtgagaacggggtt
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Pred. No. 4.2e-05;
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                                                                                                                                                   Epstein Barr Virus Nuclear Antigen 1 DNA; plasmid pCMVEBNA; EBNA 1; episome; transfection; origin of replication; EBV orif; receptor; eucaryotic host cell; recombinant cell line; ion channel; gene ther; multiple gene expression; transporter protein; transcription factor adhesion molecule; antisense therapy; gene amplification;
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98US-0130114.
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Best Local Similarity
Matches 145; Conserv
                                                                                                                                                                                                                                      This sequence represents a gene encoding a subunit of the cellulose synthese complex of Vigna angularis. The invention relates to subunits cellulose synthetic equipment, that can be used to increase the amount cellulose synthesised by a plant. The proteins and genes encoding them can also be used to improve the properties of the cellulose being produced by a plant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 789
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                             CC Insert. The invention provides a method for increasing the resistance of a core protein to proteolytic degradation that comprises linking or inserting onto or into the core protein a stabilising polypeptide of CC inserting onto or into the core protein a stabilising polypeptide of CC formula [(Glya)X(Glyb)Y(Glyc)Z]n where Glya, Glyb, Glyc are 1-6 CC sequential Gly residues and X, Y, Z are Ala, Ser, Val, Ile, Leu, Met, CC Phe, Pro or Thr and n can be anything between 1-65. X, Y and Z need not be identical from n repeat to n repeat. Alternatively a nucleic acid concoding the stabilising polypeptide can be linked onto or inserted into CC a nucleic acid encoding a core protein. The fusion proteins of the CC invention are more resistant to degradation by proteases and, thus, have CC a longer half-life than the unfused core protein. The products can be cused for treating autoimmune diseases, cancer and inflammation. In CC particular, the core protein may be an IxappaB regulator protein for the treatment of inflammatory bowel disease, or a nitroreductase protein CC which can activate nitro drugs in enzyme/prodrug therapy to treat cancer or other pathological conditions. The fusion proteins can also be used in vevo imaging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 4B; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                             New fusion proteins resistant to proteolytic degradation comprising a core protein with a stabilising polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fusion protein; stabilising polypeptide; proteolytic degradation; resistance; half-life; autoimmune disease; inflammation; nitro dr IkappaB regulator protein; inflammatory bowel disease; in vivo im nitroreductase protein; enzyme therapy; prodrug therapy; protease
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15-NOV-1996;
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RESULT NO 9221 J NO 922 J NO 9
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223778 standard;
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                                                                                                                                                                                                                                                                                                          tggagaagatcgctctgaatttggaggggtgtgccctcagccagggcagcctcaggacgg
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Pred. No. 0.00055;
0; Mismatches 248;
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Antisense; DNA library; inhibition; ss.

identification;

multiple

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Vector pShuttle DNA.

14-JAN-2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel method for generating an antisense library targeted to a selected RNA transcript. The methods can be used for identifying antisense agents and for identifying target sites for antisense mediated inhibition of a selected gene. The use of a direct library for target site selection significantly simplifies the screening process, since only very small libraries need be prepared and assayed. This sequence represents the vector pShuttle which is used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of antisense libraries, used for identifying target sites of a selected gene -
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This polynucleotide comprises the DNA sequence of vector plasmid pCMVKmITR-EPI, which contains an Epstein-Barr virus (EBV) origin of replication from plasmid pCEP4, a coding region for EBV nuclear antigen A from pCEP4, a pair of inverted terminal repeats from adeno-associated virus, a cytomegalovirus enhancer/promoter, a bovine growth hormone polyA sequence, and a kanamycin resistance selectable marker. Polynucleotides encoding polypeptides, such a crythropoletin or leptin, and ribozymes and antisense polynucleotides can be inserted into the vector. The vector is
                                                                                                                                                 Polycationic agents based on alpha-amino acids, able to complex with nucleic acid - to facilitate its entry into cell, condense and protect it against serum degradation, particularly for use
                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                           promoter
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                                                                                                                      Disclosure;
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Tetsuo U, Zukermann
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5112..6734
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polycationic agent; ss.
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                                                                                                                                                                                                                                                                                                                                                                     1173
                                                                                                                                                    G_i protein coupled receptor; G_iPCR; G_i_a protein; cytoplasmic calcium mobilization; nociceptin receptor; chemokine receptor; CCR2; interleukin 8 receptor type B; episomal expression vector;
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Pred. No. 0.000
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                                                                                                                                                                                                                 Q51731 standard;
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Pred. No. 0.00058;
D; Mismatches 248;
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Hepatocyte Growth Plasmid pCisEBON

Factor;

HGF;

mutein;

in

vitro

mutagenesis;

for subcloning huHGF variants

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Hepatocyte growth factor variants cleavage into its two-chain form, associated with HGF receptor
Example 1; F1g 6; 87pp; English
                                                                                                                                            WPI; 1993-386573/48.
                                                                                                                                                                                           Godowski
                                                                                                                                                                                                                                                                                    18-MAY-1992;
18-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                           17-MAY-1993;
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Cytomegalovirus; episomal expression plasmid; ss.
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92US-0885971
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/note* "SV40 poly I
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    are resistant to proteolytic used to treat malignancies

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18-MAY-1992;
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                                                                  18-MAY-1992;
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92US-0884811 93US-0087783 92US-0884811

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Query Match
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Matches 229
pro-hormone; beta subunit; alpha subunit; kringle domain; pr
plasminogen; catalytic domain; serine protease; HGF variant;
HGF receptor; malignancy; chronic HGF receptor activation; s
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                                                                                                                   Human; hepatocyte growth factor;
                                                                                                                                                                                        Plasmid pCisEBON for expression of hepatocyte growth factor.
                                                                                                                                                                                                                                                                         09-DEC-1996
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Pred. No. 0.00058;
0; Mismatches 248;
                                                                                                                   HGF; huHGF; serum;
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18-MAY-1992;

92US-0885971.

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This sequence represents the episomal CMV driven expression plasmid CC growth factor (HGF). HGF is isolated from human serum and is a CC disulphide linked heterodimer derived by proteolytic cleavage of the CC pro-hormone between residues 494 and 495. This generates a molecule CC composed of an alpha subunit of 440 amino acids (mol. wt. 69 kD) and CC a beta subunit of 234 amino acids (mol. wt. 34 kD). The appha and beta contains four kringle domains based on their homology to kringle-like CC domains in other proteins, e.g. prothrombin, plasminogen. The alpha subunit CC contains in other proteins, e.g. prothrombin, plasminogen. The beta CC subunit shows high homology to the catalytic domain of serine proteases. CC However two of the three residues which form the catalytic triad of CC serine proteases are not conserved in HGF. Therefore, the precise CC function of the beta chain remains unknown. The invention includes HGF covariants which retain HGF receptor binding activity without having the biological activity of wild-type HGF. They can be used for the treatment CC of pathological conditions associated with the activation of a HGF creeptor such as malignancies associated with chronic HGF receptor CC activation. The polismin comprising the HGF coding sequence confidence of the variant HGF's of the invention.
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Pred. No. 0.00058;
0; Mismatches 248;
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.
Plate: LLCM97 row: h column: 23
High quality sequence stop: 742.
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Tissue Procurement: ATCC/DCTD/DTP
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NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammallan
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Best Local Similarity
Matches 626; Conserv
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GTGGCTGTTTCCTCTGCGAGAACCAGGAGTGAACTGGCATGCCAAGCCCCTCACGCTCAG
                                                                                    9t99ct9tttcctctgcgagaaccaggagtgaactggcatgccaagcccctcacgctcag 488
                                                                                                                                          CATTCTTCAGAACTGGACGGACAACTATGACCTCCTTGAGGACAATCACTCCTACATCCA
                                                                                                                                                            cattetteagaaetggaeggaeaaetatgaeeteettgaggaeaateaeteetaeateea 428
                                                                                                                                                                                                                                 amacctgagtttctacagamatgagatccgcttcctgcccamacggctgtttcattgagga 368
                                                                                                                                                                                                                                                                                                     gtgtmggtmtcggcacmactmtccggmtctggtggmacgmgagactgcmatggggmacacgcc
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Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
plate: LLCM286 row: 1 column: 17
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Contact: Robert Strausberg,
Tel: (301) 496-1550
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/tlssue_type="melanottc melanoma"
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/lab_host="DH10B (phage-resistant)"
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/note="Corgan: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Corgan: skin; Vector: pOTB7; Site_1: XhoI; Site_2: Corgan: skin; Vector: potential for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
70 a 202 c 254 g 125 t
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/db_xref="taxon:9606"
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Pred. No. 7.4e-111;
0; Mismatches 19;
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Best Local Sin
Matches 654;
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CGAGGAGTCGGAGGAGCCGCGGCGGCGCGCCCAGCTCCAGTCCAGAATGACAGG
                 cgaggagtcggaggagccgcgggcgcgggcccagctcgttccagtccagaatgacagg
                                                                    gagcacagaactaccagaagcgcttccagaacctgaactggcgcagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM288 row: j column: 11
High quality sequence start: 20
High quality sequence stop: 663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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601278145F1 NIH_MGC_20
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EST.
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                                                                                                                                                                                                                   Similarity 96.:
54; Conservative
                                                                                                                                                                                                                                                                                                                               160
                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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/cored; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5;
adaptor: GGCAGGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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                                                                                                                                                                                                                 Score 586; DB 35;
Pred. No. 1.6e-109;
0; Mismatches 20;
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AW338856 AW338856 1 GI:6835482
                                                                                                                                                                                                                                                                                                                                                                                                                 CTGGAGGACCGAGGCACGGGCACCGGTGGGCCGAGCACAGAACTACCAGAAGCGCTTTCA
                                                                     Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
seq primer: -40UP from Gibco
                                                                                                                                                        Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 606)
                                                                                                                                                                                                                       Homo sapiens
                                                     quality sequence stop: 421.
Location/Qualifiers
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                                                                                                                                                                                                                                                                           mRNA EST 31-JAN-2000
1 Homo sapiens cDNA clone IMAGE:2878779
6029 7-60. ;contains element MSR1 repeti
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Mammalla; Eutheria; Pri
1 (bases 1 to 522)
1 (bases 1 to 522)
Koehrer, K., Beyer, A., M
EST (Koehrer, et al.)
Unpublished (1999)
Contact: Koehrer K
MIPS
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DKFZp762B143_r1 762 (s
DKFZp762B143 5', mRNA
AL120919
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Similarity 97.1%;
40; Conservative
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Site_2: Not1; Cloned unidirectionally. Primer: Oligo of
Average insert size 1.72 kb. Life Technologies catalog
11548-013"
a 195 c 204 g 111 t 3 others
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3; Mismatches 11;
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AW732857 526 bp mRNA EST 21-APR-200 bb15g10.yl NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963010 similar to TR:096029 096029 7-60.;, mRNA sequence.
AW732857 AW732857.1 GI:7633196 EST.
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No. s1 sequence available.
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Location/Qualifiers
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/clone_11b="762 (synonym: hmel2)"
/tissue_type="melanoma (MeWo cell 1:
/dev_stage="adult"
/lab_host="bH10B"
/note="Vector: pSport1; Site_1: Not:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC
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Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
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NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian
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/clone="IMANGE:2963010"
/clone=lib="NIH_MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage resistant)"
/lab_host="DH10B (phage resistant)"
/lab_host="DH10B (phage resistant)"
/note="Organ: placenta; Vector: pOTB7; Site_1: xhoI;
Site_2: ECORI; CDNA made by oligo-dT priming.
Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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gccacgagggacatgtgtaggtatcggcacaactatccggatctggtggaacgagactgc
                              CCGCGGGCGCGCCCCAGCTCGTTCCAGTCCAGAATGACAGGGTCCAGAAACTGGCGA
                                               | ccgcgggcggcgcggcccagctcgttccagtccagaatgacagggtccagaaactggcga
                                                                                        TCCATGTGTGAGGAGGACGAGGATGCGGAGGACGCGGGGACGACGACGACTGCGAGGAC 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: image.llnl. Plate: LLCM337 row: f column: 03 High quality sequence start: 95 High quality sequence stop: 591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 591)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection
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601303311F1 NIH_MGC_21 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                         136
                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                 /Organism="Homo sapiens"
//db_xref="taxon:9606"
//clone="IMAGE:3637634"
//clone=lib="NIH_MGC_21"
//tissue_type="choriocarcinoma"
//lab_host="PH10B (phage-resistant)"
//lab_host="PH10B (phage-resistant)"
//note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: ECORI; CDNA made by oligo-dT priming.
Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
36 a 149 c 196 g 109 t l others
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IMAGE:3637634
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ba97e12.y1
similar to
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Seq.primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       National Institutes of Health, Mammalian Unpublished (1999) Other_ESTs: ba9712.x1
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1 (bases 1 to 493)
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              103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quality sequence stop: 423.
//tissue_type="renal_cell adenocarcinoma"
//lab_host="DH10B (phage-resistant)"
//note="Organ: kidney; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
03 a 150 c 186 g 53 t 1 others
                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2957902"
/clone_lib="NIH_MGC_14"
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Primates;
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Emmail: Robert_Strausberg@nih.gov

Tissue Procurement: ATCC/DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Cone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

WMW-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40Up from Gibco

High quality sequence stop: 434.

Location/Qualifiers

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 551)
1 (bases 1 to 551)
1 NH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Vopublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                             BE207411 551 bp mRNA ba66d10.x1 NIH_MGC_20 Homo sapiens cDNA similar to TR:096029 096029 7-60.;, mRN BE207411 GI:8750809
                                                                                                                                                                                                                                                                                                                                                                 human
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 3.5e-87;
0; Mismatches 4;
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Best Local Sim
Matches 476;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 529)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collec Unpublished (1999)
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/clone_lib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/lab_host="DH1D8 (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, BerKeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
96 a 1/5 c 180 g 100 t
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Pred. No. 3.9e
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łomo sapiens
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.9e-85;
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                                                                                                                                                       aagataggccggagcccttaagccccaaagagagcaagaagaggaagctggagctggagcc 1204
                                                                                                                                                                                                                                                                                                                                                                                                                              agctgcggaggttcaagcccagctctctgccccatccgctcgagggctccaggaaggtgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tycacttcycctygyaycacttccyyccccyctycaayttcytctygygyccccaayaca
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                                                                                                                                                                                                                                                                                                                             GCCCAGAGCATAGCAAGGGTGGGGGCA-GGTGGACGAGGGGCCCCCAGCCACGGAGCGTGG
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                                                                                                                                                                                                                              AGCCCCAGGATGCGGGACCCCTGGAGAGGAGCCA-GGGGATGAGGCAGGGGGCCCACGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCTGCGGAGGTTCAAGCCCAGCTCTCTGCCCCATCCGCTCGAGGGCTCCAGGAAGGTGG
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                                                                                                                             AAGATAGGCCGGAGCCCTTAAGCCCCCAAAGAGAGCAAGAAGAGGAAGCTGGAGCTGAGCC
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Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Prayad by: The I.M.A.G.E. Consortium ()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE: 5820767"
/clone="IMAGE: 5820767"
/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage=resistant)"
/lab_host="Plantant"
/lab_host=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 6.7e-83;
0; Mismatches 3
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caaggcgggggaggcagcagagttgcagkacgcagaggtggagtcttctgccaagtctgg 1997
                                                                                                                       cyagageceateggagaececaggeeceageeeggeaggaeetacaagggatgageeage 1937
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                                                                                          CGAGAGCCCATCGGAGACCNCAGGCCCCAGCCCGGCAGGACNTACAAGGGATGAGCCAGC
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national Institutes of Health, Mammallan of
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Other_ESTs: 2821312.5prime
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Email: Robert_Strausberg@nih.gov
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/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; CDNA made by oligo-dT priming. Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rublin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 173 c 174 g 105 t 2 others
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/cell_line="MGC3"
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/db_xref="taxon:9606"
/clone="IMAGE:2821312"
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                                                                                                                                                                                                                                                                                             http://www.genome.washington.edu
Plate: LLCM6 row: H column: 17
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Email: Robert_Strausberg@nih.gov
Tissue Procurement: DCTD/DTP cDNA
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Other_ESTs: 2821312.3prime
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/clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
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/db_xref="taxon:9606"
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High quality sequence start: 2
High quality sequence stop: 532.
Location/Qualifiers
                             CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: image.l Plate: LLCM317 row: e column: 21 High quality sequence start: 2
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National Institutes of Health, Mammalian (
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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601299883F1 NIH_MGC_21
                                                                                                                                     Tissue Procurement: ATCC
                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1296)
                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
BE409569
                                                                                                                                                                                                                                                                                                                               BE409569.1 GI:9346019
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                                                                                                                                                                                                                                                                                                                                                                          Homo
                                                                                                                                                                                                                                                                                                                                                                         sapiens
                                                                                                                                                                                                                                                                                                                                                                         CDNA
                                                                                                                                                                                                           Gene
                                                                                                                                                                                                                                                                                                                                                                         clone
                                                                                                                                                                                                                                                      Hominidae;
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IMAGE:3629948 5',
                                                         imation can be image.llnl.gov
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BASE COUNT
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Best Local Similarity
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              ggcgggagcagccgcccacagagccaggccctcagagtgcctcagaggtggagaagatcg 1264
                                                                                                                                                                                                                                                                                                                                                                                                gtgtgagctgagcctcgagcacttccaggcgccactggtccgcttcttcctggaggagac 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ccagaacctgaactggcgcagccacaacaacctccgcatcacacgcatcctcaagtcgcc 692
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                                                                                                                                                                               999acccctggagaggagccaggggga---tgaggcaggggggccacgggggaagataggcc 1154
                                                                                                                                                                                                                                                          gggtgggggcaggggtggacgagggccccaggcacggagcgtggagccccagg---atgc 1097
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                                                                              GCAGGAGCCCATATACGCACGAAACAGAGACGCAGCACGAAAAGATGGCGCCTGACCC
                                                                                                                   ggag----
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/db_xref="taxon:9606"
/clone=lib="NHL_MGC_21"
/clone_lib="NHL_MGC_21"
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/inote="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
27 a 416 c 389 g 164 t
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                                                                                                     19.4%;
84.7%;
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Pred. No. 1.6e-80;
O; Mismatches 89;
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VERSION
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SOURCE
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Best Local Similarity
Matches 577; Conserv
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| ||||| ||
                    ggcgagccacgagggacatgtgta-ggtatcggcacaactatccgga-tctggtggaacg
                                                                                                                                                                            CAATTCACACTGGGAGGACGAGGAGGAGGATGCGGATGACGCGGAGGACTGCGA 153
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GGCGAGCCACGAGGGACATGTGTACGGTATCGGCACAACTATCCGGATTCTGGTGGAACG
                                                                            GGAGCCGCGGGCGGACGCGTCCCATCTCGTTCCAGTCCAGAATGACAGGGTCCAGAAACT
                                                                                                CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM252 row: f column: 03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
BE391750
BE391750.1 GI:9337115
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601283311F1 NIH_MGC_44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
1 (bases 1 to 757)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE::5604994"
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/lab_host="DHIOB (phage-resistant)"
/note="OCRITY DHIOB (phage-resistant)"
/note="OCRITY DHIOB (phage-resistant)
/totalional into EcoRITY DHIOB (priming. Directionally
cloned into EcoRITY DHIOB (sites using the following 5,
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
70 a 204 c 251 g 131 t 1 others
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                 19.0%;
                                                                                                                                                                                                                                                                                                                Score 435.4; DB 35;
Pred. No. 7.2e-79;
0; Mismatches 31;
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             612.6
547.8
302
91.2
85.2
80.8
75.8
72.4
71.2
68.2
68.2
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1: /SIDS1/gcgdai
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10: /SIDS1/gcgdai
11: /SIDS1/gcgd
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22.7 802
12.5 3.8 114955
3.8 114955
3.1 1789
3.1 789
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3.0 10732
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Prostate cancer as Prostate cancer as EST clone BK517.
Human adenosine Al Human adenosine Al DNA encoding antig Prostate cancer as Gene encoding a su Epstein Barr Virus KSHV long unique c Nucleotide sequenc.
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Human lung tumour		20		2.2	54	45
HC	Q39212	14		2.3	4	44
		20		2.3	4	43
Human prostate pro		18		2.3	54.8	42
Human colon cancer	A02504	21		2.3	5	41
Human colon cancer		21		2.3	5	40
	N90579	10		2.3	5	
Partial mouse WRN		18	16442	2.3	56	c 38
Human telomerase p		19		2.3	Q	37
Homo sapiens mamma		19		2.3	56.2	36
Human adenosine re		21		2.4	7	
		20	6225	2.4	7	
		σ	600	2.4	7	c 33
Partial mouse WRN		18	51259	2.4	æ	
Mouse histone H2B		20	150	2.4	æ	31
Human gene express		20	1337		æ	
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ain SB5		19	117213		60	
KSHV long unique c		19	137507		60.2	
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Leishmania donovan		16	1091		60.4	
Human colon cancer		21	1218	2.5	61.2	24
DNA encoding Pseud		15	8438		61.8	23
PCR primer for 5'		14	390		62.6	22
Randomising oligon		13	390		62.6	21
FLGA insert stabil		19	795		64	20
μ.		20	10596		7	19
	T40348	17	10596		7	18
	Q51731	14	10596		7	17
Nucleotide sequenc	222248	20	10380		7	16
	V21683	19	9600		67.2	15
r pShu	Z23778	20	8705		7	c 14
Anti-sense strand	092	20	5452		7	c 13

ALIGNMENTS

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22-JUN-1998;
17-JUL-1997;
10-OCT-1997;
10-OCT-1997;
10-OCT-1997;
11-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                Cancer associated antigen; diagnosis; research; treatment; human;
breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
                                Chen Y,
Tureci 0;
                 Pfreundschuh M,
                                                               (LUDW-) LUDWIG INST CANCER RES.
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97US-0061765.
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The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast
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Best Local Sin
Matches 302;
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                                                                                                                                                                                                                                                                                                                                                2107
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The specification describes antisense oligonucleotides (X52869-X55271) CC directed against at least 2 mRNAs selected from target genes, coding and connecoding regions of RNAs corresponding to target genes, gene coninitation codons, genomic flanking regions, intron-exon borders, the CC initiation codons, genomic flanking regions, intron-exon borders, the CC regions and all segments of RNAs encoding proteins associated with one CC or more diseases, conditions or mixtures. The antisense oligonucleotides (apecifically X55100-271) can be used for the antisense CC may be derived from sequences X55272-74. These multiple target coligonucleotides (apecifically X55100-271) can be used for the antisense CC treatment of diseases and conditions. Typical diseases and conditions conditions continuing lung diseases, pulmonary vasconstriction, inflammation, CC including lung diseases, pulmonary vasconstriction, inflammation, callergic rhinitis, acute asthma, allergies, asthma, impeded respiration, callergic rhinitis, acute asthma, allergies, asthma, pulmonary cancer your constriction, emphysema, chronic obstructive cultumonary disease (COPD), and cancers such as leukemias, pulmonary cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic cunetastases, as well as all types of cancers, melanoma, hepatic cancer, metastasize to the lungs, including breast and prostate cancer.
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Best Local Similarity
Matches 534; Conser
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chronic obstructive pulmonary disease; leukemia; lymphoma; c
colon cancer; breast cancer; lung cancer; pancreatic cancer;
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 New antisense oligonucleotides used in treatment of,
                         WPI; 1999-229400/19
                                                                                                   09-JUN-1998;
17-SEP-1997;
                                                                                                                                      17-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The specification describes antisense oligonucleotides (X52869-X55271) CC directed against at least 2 mRNAs selected from target genes, coding and cc non-coding regions of RNAs corresponding to target genes, gene cc initiation codons, genomic flanking regions, intron-exon borders, the cc french the 3'-end and the juxta-section between coding and non-coding cr regions and all segments of RNAs encoding proteins associated with one cc may be derived from sequences X55272-74. These multiple target coligonucleotides (specifically X55180-271) can be used for the antisense cligonucleotides (specifically X55180-271) can be used for the antisense cr reatment of diseases and conditions. Typical diseases and conditions care those associated with impaired respiration and inflammation, cc ancer those associated with impaired respiration and inflammation, cc allergic rhinitis, acute asthma, allergies, asthma, impeded respiration, respiratory diseases, pulmonary vasoconstriction, inflammation, callergic rhinitis, acute asthma, cystic fibrosis, pulmonary compartatory diseases (COPD), and cancers such as leukemias, lymphomas, cc carcinomas eg. colon cancer, breast cancer, lung cancer, hepatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic concerts, hepatocellular carcinoma, kidney cancer, melanoma, hepatic concerts, as well as all types of cancers which may metastasize or have concerts as a concert cancer.
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                                                                         interaction between the agent and the NAM or the expression product as determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human brea cancer, renal cancer, colon cancer, gastric cancer, prostate cancer an
                                                                                                                                                                                  The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cancer
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                                                               This sequence represents a gene encoding a subunit of the cellulose synthase complex of Vigna angularis. The invention relates to subunits cellulose synthetic equipment, that can be used to increase the amount cellulose synthesised by a plant. The proteins and genes encoding them called be used to improve the properties of the cellulose being
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Pred. No. 9.6e-05;
D; Mismatches 248;
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CK (SHV is a new human Herpesvirus (HHV8) believed to cause Kaposi's sarcoma (KS) which is the most common form of neoplasm occurring in persons with acquired immune deficiency syndrome (AIDS). The DHFR protein is useful for vaccination, prophylaxis, diagnosis and treatment of a subject with Kaposi's sarcoma in a call
                                                                                                                                            Query Match
Best Local
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   24367
                                 1653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dihydrofolate reductase; LUR; long unique region; vaccine; prophylaxis diagnosis; treatment; HHV8; complement binding protein; v-CBP; SSBP; ssDNA binding protein; transport protein; glycoprotein B; pol; vIL-6; DNA polymerase; viral interleukin-6; BHV4-IE1 I; thymidylate synthase; vMIP-II; BHV4-IE1 II; vMIP-I; capsid protein I; tegument protein I; ds
                                                                                                                                                                                                          Sequence 35100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               di:hydro:folate reductase and
or diagnosis of Kaposi's sarce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaposi's sarcoma-associated herpes virus nucleic acid - di:hydro:folate reductase and is useful for treatment, p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V73802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V73802 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Column 67-96; 109pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bohenzky RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYCO ) UNIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaposi's sarcoma-associated herpesvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSHV LUR DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-FEB-1999
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                   gaccccaggccccagcccggcaggacctacaagggatgagcccagccgagagcccatcgga
                                                                               Kaposi's
Similarity
                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (nucleotides 1-35,100).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chang Y,
                                                                                                                                                                                                                                         sarcoma in a cell.
                                                                                                                                                                                                          BP; 8703 A; 9395 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0770379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acquired immune deficiency syndrome;
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                                                                                                                                            . 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sarcoma
                                                                                                                             0
                                                                                                                                            Score 68.2; DB 20; Pred. No. 0.00042;
                                                                                                                             Mismatches
                                                                                                                                                                                                          8921 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Moore PS,
                                                                                                                                                                                                          8081 T;
                                                                                                                             238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Russo
                                                                                                                             Indels
                                                                                                                                                           Length
                                                                                                                                                                                                           0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIDS;
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RESULT 11
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ID 941
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XX KSHV 1
COS ETT CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                             KSHV; HHV8; human herpes virus 8; macrophage inflammatory protein II; interleukin-6; II-6; interferon regulatory factor; rheumatoid arthritis; complement-binding protein; glycoprotein; capsid protein IV; infection; immediate early protein; Kaposi's sarcoma; protective vaccine; lymphoma; lymphoprolliferative disease; leukaemia; splenomegaly; mycosis fungoides; HIV immune status; anti-inflammatory agent; therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                 Kaposi's sarcoma-associated herpes virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V19941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        V19941 standard; DNA; 137507 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KSHV long unique coding region and terminal repeat
                                                                                                                                                                                                                                                                                                                                                                                                                           immune status; anti-inflammatory agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99a99999atcccggcgccaccctccccggaggggatcccggcgccc
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                                                                                                          /product= protein T1.1 complement (58976..60175)
                                                                                                                                                                                                                                                                                                                   /*tag= a
/product= complement-binding protein
8699..11236
                           /product= glycoprotein L
complement (88410..88910)
                                                                                                                                                    28661..29741
                                                                                                                                                                                         /product- macrophage inflammatory protein complement (27137..27424)
                                                                                                                                                                                                                                 /product= interleukin 6
complement (21548..21832)
                                                                                                                                                                                                                                                                         /product= glycoprotein B complement (17261..17875)
                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                   glycoprotein M
t (69412..69915)
                                                                                                                                                               interferon regulatory factor
interferon regulatory factor
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                                                                                                                                                                                                                                                                                                                                                                                                                            therapy;
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CC This sequence represents the long unique region and terminal repeat of CC the Kaposi's sarcoma-associated herpes virus (KSHY). KSHY is also known CC as human herpes virus 8 (HHV8). This sequence contains the DNAs of the CI invention which encode KSHY polypeptides selected from: (a) viral CC (a) viral IRF 1; (d) complement-binding protein; glycoproteins B, M or L; (d) capsid protein IV encoded by ORF65; and (e) immediate early protein CC encoded by ORF73. Labelled probes for the nucleic acid, proteins encoded by it, and antibodies (Ab) specific for the proteins are useful for CC detecting HHV8, specifically for diagnosis of Kaposi's sarcoma, in body CC fluids or tissue samples. HHV8 infections can be treated with antisense CC or triplex forming molecules or agents that bind specifically to the protein. Ab may be used for prophylaxis or treatment of HHV8 infection, CC while the protein can be used in protective vaccines. Ab may also be used to differentiate between lymphomas, and HHV8 may be implicated in many CC other lymphoproliferative diseases such as lymphomas, leukaemia, splenomegaly and mycosis fungoides. Cells and animals containing the CC nucleic acid are useful for drug screening. HHV8-derived peptides can be used as targets for antiviral drugs, e.g. dihydrofolate reductase gene CC can be inhibited with methotrexate. These can also be used to determine the immune status of a patient infected with HIV. HHV8 derived protein cc. g. treating rhemacs an anti-inflammatory agent for, craft of the protein and secure is stated as containing containing the secure of the immune status of a patient infected with HIV. HHV8 derived protein cc. g. treating rhemacs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JUL-1996;
25-JUL-1996;
05-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding Kaposi's sarcoma associated herpes proteins - useful for, e.g. detecting levels of HHV8 in, and preparation of vaccines for treatment of, HIV patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example
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25-JUL-1996;
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25-JUL-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Page 135-203; 230pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chang Y,
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96US-0688814.
96US-0708678.
96US-0728323.
96US-0747887.
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complement (93636..94127)
/*tag= 1
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/product= interferon regulatory factor 3
90173..90643
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complement (111931..112443)
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complement (123808..127296)
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Sequence 137507

BP; 32579

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G; 31375 T; 0 other;

Disclosure;

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V65831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2013
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New fusion proteins resistant to proteolytic degradation comprising a core protein with a stabilising polypeptide a peptide sequence containing glycine repeats
                                                                                                                                                                                                                                        25-JUN-1997;
15-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                              28-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Epstein-barr virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide sequence of the stabilising sequence-encoding insert.
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                                                                                                WPI; 1998-312463/27
                                                                                                                                                                                                                                                                                                               17-NOV-1997;
                                                                                                                                                                                           (MASU/) MASUCCI
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hes 227;
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96US-0030986.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stabilising polypeptide; proteolytic degradation
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Pred. No. 0.00048;
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                           comprising
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CC This is a nucleotide sequence of the stabilising sequence-encoding CC insert. The invention provides a method for increasing the resistance of a core protein to proteolytic degradation that comprises linking or inserting onto or into the core protein a stabilising polypeptide of CC formula [(Glya)X(Glyb)Y(Glyc)2]n where Glya, Glyb, Glyc are 1-6 CC sequential Gly residues and X, Y, Z are Ala, Ser, Val, Ile, Leu, Met, CC Phe, Pro or Thr and n can be anything between 1-66. X, Y and Z need not CC encoding the stabilising polypeptide can be linked onto or inserted into CC a nucleic acid encoding a core protein. The fusion proteins of the CC invention are more resistant to degradation by protease and, thus, have CC alonger half-life than the unfused core protein. The products can be CC used for treating autoimmune diseases, cancer and inflammation. In CC particular, the core protein may be an IkappaB regulator protein for the CC treatment of inflammatory bowel disease, or a nitroreductase protein CC which can activate nitro drugs in enzyme/prodrug therapy to treat cancer CC or other pathological conditions. The fusion proteins can also be used in CC diagnostic methods such as in vivo imaging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fig
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Sequence

799 BP; 201 A; 106 C; 479 G; 13. T; 0 other;

RESULT 13 X90923/c 멍 Ş 밁 δÃ 밁 Q 밁 δÃ 밁 Q 멁 8 밁 XXXXXXXXX δÃ Matches Query Match 1193 1073 1016 1133 X90923 X90923 1313 1253 142 502 382 262 956 ggaaggtggaggaaggaagccccgggggacccccgaccacgaggccagcacccagggtc 1015 Local 9gacctgtgagccagagcatagcaagggtgg---gggcagggtggacgagggggccccagc 1072 tgggagccagggtggccgacaaggtgaggaagcggaggaaggtggatgagggtactgggg ggacccaggaagtgggcggtcaggaccctggggaggcagtgcagccctgccgccaacccc ggggccacggggaagataggccggagcccttaagccccaaagaggaagcaagaagaagc 1192 cacggagcgtggagccccaggatgcggggacccctggagaggaggccagggggatgaggcag <u>адудусаддадсаддадудсаддадсаддадудсаддадсаддаддесаддадсадда</u> tggagaagatcgctctgaatttggagggtgtgccctcagccagggcagcctcaggacgg 1312 <u>адуудсаддадуусаддадуудсаддадсаддаддадууссаддадсаддадсаддадсадд</u> tggagctgagccggggggagcagcccacaggggccatggcctcagagtgcctcagagg адуадсаддаддаддосаддадддосаддадсаддаддаддддсаддадддсаддадд 229; standard; Similarity Conservative DNA; 2.88; 0 Score 67.2; DB 19; Pred. No. 0.00047; 0; Mismatches 248; Indels Length 799; ω Gaps 1132 1252 561 441 381 321 261 201 ۲.

Anti-sense strand; plasmid pCMVEBNA; EBNA 1;

episome;

transfection;

Anti-sense strand of pCMVEBNA plasmid

17-JAN-2000

(first entry)

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Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                        Matches
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       1918
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                                                                                                                                                                                                                                                                                          2098
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06-AUG-1998;
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Cytomegalovirus.
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Local Similarity 47.7%;
es 229; Conservative
                                  9999ccac9999aagataggccggagcccttaagccccaaagagagagcaagaagaggaagc
                                                                                                                         cacggagcgtggagccccaggatgcggggacccctggagaggaggccagggggatgaggcag
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ggaaggtggaggaggaaggaagccccggggaccccgaccacgaggccagcacccagggtc 1015
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98US-0130114
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Pred. No. 0.00055;
0; Mismatches 248;
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ggaaggtggaggaaggaagccccgggggaccccgaccacgaggccagcacccagggtc 1015

Query Match Best Local s Matches 229

Similarity

2.8%;

9: Score 67.2; D 9: Pred. No. 0.00 0; Mismatches

DB 20;

Length

8705;

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229;

Sequence 8705 BP;

1875 A; 2575

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                                                                                                                                         Production agents and inhibition
                   This invention describes a novel method for generating an antisense library targeted to a selected RNA transcript. The methods can be used for identifying antisense agents and for identifying target sites for antisense-mediated inhibition of a selected gene. The use of a direct library for target site selection significantly simplifies the screening process, since only very small libraries need be prepared and assayed. This sequence represents the vector pShuttle which is used in the method of the invention.
                                                                                                                  Claim 16; Page 43-50; 63pp; English
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06-NOV-1998;
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                                                                                                                                        of antisense libraries, for identifying target s of a selected gene -
                                                                                                                                                                                                                                                                                                                                                                                 DNA library; identification; multiple cloning
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98US-0107504.
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       19-FEB-1998
                                                                                                                                               repeat_unit
                                                                                                                                                                        misc_feature
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                        WO9806437-A2
                                                                                promoter
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                                                        terminator
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                                                                                                                                                                                                                                Adeno-associated Cytomegalovirus.
                                                                                                                                                                                                                                                Epstein-Barr virus
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                                                                                                                                                                                                                                                                vaccine;
                                                                                                                                                                                                                                                                       delivery; plasmid pCMVKmITR-EPI;
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/note= "EBV (
4928..5104
                                                                                                                                                                                                                         taurus
                                                                                                                                                                       /product= '2623..4559
                                                       /note= "CMV immediate-early enhancer/promoter" 6818..7050
                                                                               5112..6734
                                                                                                                       /rpt_type= ]
/note= "AAV
                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polynucleotides can be inserted into the vector. The vector is preferred for use in novel compositions and methods for improved polynucleotide delivery into cells. In these methods, polycationic agents are used to increase the frequency of uptake of a nucleic acid (see also V21684-86) into a cell. The polycationic agent can condense with the nucleic acid and inhibit serum and/or nuclease degradation of the nucleic acid. The nucleic acid can be a vector, may express a therapeutic protein or a vaccinating viral or cancer antigen, or is itself therapeutic (antisense or ribozyme). The methods and compositions can be used in the gene therapy of many diseases.
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KmITR-EPI, which contains an Epstein-Barr virus (EBV) origin
eplication from plasmid pCEP4, a coding region for EBV nuclea
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Page 14

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ctctctgccgcatccgc 943 	gttcgccgtgcgctgcc 823		CGGGATCCGGCTGGAGG 60 CGGGATCCGGCTGGAGG 60 gcgcttccagaacctga 643	ກ່າວ	rtructed by Ling Hong in (University of or one in the synthesis kit RT (Life Technologies)."				Gene Collection (MGC)	EST 13-JUL-2000 clone IMAGE:3536657 5', Vertebrata; Euteleostomi; i; Hominidae; Homo.

Result No.

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JOURNAL COMMENT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 868)

NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM97 row: h column: 23 High quality sequence stop: 742.
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Tissue Procurement: ATCC/DCTD/DTP
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BE277227.1 GI:9152194
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                                                                                                                                                                                            171
                                                                    Conservative
                                                                                                                                                                                   /db_xref="taxon:9606"
/db_xref="taxon:9606"
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cloned into EcoRI/XhoI sites using the following 5/
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insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
71 a 245 c 294 g 157 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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                                                                                     24.8%;
88.1%;
                                                               Score 596.6; DB 34;
Pred. No. 5.6e-111;
0; Mismatches 74;
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                                                                                                         Length
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REFERENCE
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DEFINITION
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		863	GGGCCC	TGGGAGCCT	841	₽
		877	ggccc	tgggagcacttc	855	Qγ
	TGCCAGCTGGTTGCCCTC	TGCCGACA	GETCGCCGTGCGC	GACTTACTTCATGO	781	В
gc 854	cgccagctggtgca	tgccgacaccagcg	ttegeegtgeg	cttcat	797	VΩ
3G 780	GTGCCGGCAGA	CGGTGAGCTGCCGGGGG	GGAGACGCTGGTGCGGG	CTGGAGGGAGACGC	721	В
gg 796	tgcggcagagtgc	cgggagctgccgggg	ctggtgcgg	tgga-	742	γQ
rc 720	GCCGCTGGGTCCGCTTC	CGAGCACTTCCAG	AGCTGGG	AAGTCGCTGGGT	661	뭥
tc 741	cgccactggtccgcttctt	tcgagcacttccagg	gagctgagcct	caagtcgccgtgtg	684	Qy
CT 660	AGCGCTTCCAGAACTGGCGCAGCCACCAACAACCTCCGCATCACACGCATCC	GGCGCAGCCACAACAAC	AACCTGAACT	GAAGCGCTTCCAG!	601	ф
ct 683	ctccgcatcacacgcatc	ggcgcagccacaacaac	acctgaact	- Oi	624	Ϋ́
CA 600	GGCCGAGCACAGAACTAC	CTGGAGGACCGAGGCACGGCACGGTG	CTGGAGGACCC	ACGGGGATCCGG	541	g
ca 623	ggccgagcacagaactac	gaggcacgggcacggtg	ctggaggaccg	c-gggatccgg	565	Qy
rC 540	GCCTACGAGCTCATGCTGGGCTT	CTCCCAGGAGATCCAGGAGCGGCTTGTCCGGGCCT	AGATCCAGGAC	AAAAGCTCCCAGG/	481	B
tc 564		gcggcttgtccgggcct	agatccaggag		505	Qγ
TT 480	TCAGGGAGGTCGAGGTGTT	CAGGAGTGAACTGGCATGCCAAGCCCCTCACGCTCAGGGAG	IGAACIGGCAI	CGAGAACCAGGAG	421	В
tt 504	gtcgaggtg	tgccaagcccctcacgc	tgaactggcat	gagaac	445	Qy
IG 420	TCCAGTGGCTGTTTCCTCTG	GGACAATCACTCCTACATCCAGTGG	ACCTCCTTGAC	ACGGACAACTATGACCTCCTTGAG	361	В
tg 444	tccagtggctgtttcctc	ggacaatcactcctaca	acctccttgag	acggacaactatga	385	δĀ
	CTTCAGAACT	GAAATGAGATCCGCTTCCTGCCCAACGGCTGTTTCATTGAGGACATT	CTTCCTGCCC	AGAAATGAGATCCC	301	용
gg 384	cttcagaact	caacggctgtttcattg	getteetgee	agaaatgagatcc	325	δÃ
AC 300	ACGCCAAACCTGAGTTTCT	CAGACTGCAATGGGGACA	GETGGAAC	AACTATCCGGATCT	241	뭥
ac 324	gccaaacctgagtttct	actgcaatggggac	ggtggaac	ctatccgga	265	Qy
AC 240	ACATGTGTAGGTATCGGC	TTGGCGAGCCACGAGGG	STCCAGAAAC	CCAGAATGACAGG	181	뭥
ac 264	-tggcgagccacgagggacatgtgtaggtatcggcac	-tggcgagccacgaggg	gtccagaaac.	ccagaatgacagggtccagaaac	206	Qy
GT 180	GCGGCCCAGCTCGTTCCA	ATGCCTGCGTGGCGGCT	TCGGATGG	TGAGGACGATGGATG	121	В
gt 205	geggeecagetegtteea	gagccgcgggcg	aggagtcg	-10	146	VΩ
AC 120	īG	GCCTGGCGCTGAGGTGA	CCI	ACTGCTGAGGACGGCGATGG	61	뭣
cg 145	gcgagggacgcgga	gc	gcgaggcc	ctgc	104	Qγ
3G 60	CGGAGGACGCGGAGGACGAG	ACGAGGAGGATG	CACCTGGGAG	CCGACTGCGACTCCACCTGGGAGGAGG	1	8

Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 751) NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

mRNA sequence. BE387193

BE387193.1 EST. human.

GI:9332558

BE387193 751 bp 601277069F1 NIH_MGC_20

mRNA Homo

sapiens cDNA

21-JUL-2000 clone IMAGE:3618136

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                                   ggaggtcgaggtgtttaaaagctcccaggagatccaggagcggcttgtccgggcctacga
                                                                                                                                                                                                                           CATTCTTCAGAACTGGACGGACAACTATGACCTCCTTGAGGACAATCACTCCTACATCCA
                                                                                                               GTGGCTGTTTCCTCTGCGAGAACCAGGAGTGAACTGGCATGCCAAGCCCCTCACGCTCAG
                                                                                                                                               cattcttcagaactggacggacaactatgacctccttgaggacaatcactcctacatcca
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGTAGGTATCGGCACAACTATCCGGATCTGGTGGAACGAGACTGCAATGGGGACACGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCCAGCTCGTTCCAGTCCAGAATGACAGGGTCCAGAAACTGGCGAGCCACGAGGGACAT
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Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
plate: LLCM286 row: 1 column: 17
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High quality sequence stop: 727.
Location/Qualifiers
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//organism="Notation of Site_2: XhoI; Site_2: XhoI; Site_3: XhoI; Site_3
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Pred. No. 3.6e-110;
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cgaggagtcggaggagccgcgggcgggcgcggcccagctcgttccagtccagaatgacagg 218
                                                                              CGAGGACTGCGAGGACGGCGAGGCCGCCGGCGGCGAGGGACGCAGGGACGAGGA
                                                                                                  cgaggactgcgaggacggcgaggccgccggcggagggacgcggagggacgcaggggacgagga 158
                                                                                                                                                      GACCCGTAGTGCGAGTCCACCATGGGAGGAGGAGGAGGAGGATGCGGAGGACGCGGAGGA
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1 (bases 1 to 682)

NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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601278145F1 NIH_MGC_20
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                         /tissue_type="melanotic melanoma"
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cloned into EcoRI/XhoI sites using the following 5/
adaptor: GCCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZaP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
60 a 190 c 224 g 108 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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                                                          Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 606)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert-Strausberg@nih.gov

Life Technologies catalog #: 11548-013

DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.lini.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco
High quality sequence stop: 421.

Scarior Consortium/CLNL at:

Location/Qualifiers
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AW338856 AW338856 1 GI:6835482
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/organism-"Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2878779"
/clone_lib-"NCI_CGAP_Pan1"
/tissue_type="adenocarcinoma"
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                                                                                                                                                                              AL120919 522 bp mRNA
DKFZp762B143_r1 762 (synonym:
DKFZp762B143 5', mRNA sequence
AL1120919
                          Koehrer, K., Beyer, A.,
EST (Koehrer, et al.)
Unpublished (1999)
Contact: Koehrer K
                                                                               Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 522)
                                                                                                                          Homo sapiens
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/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: St
Site_2: Not1; Cloned unidirectionally. Primer: Oligo of the primer size 1.72 kb. Life Technologies catalog 11548-013"
195 c 204 g 111 t 3 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone (DKEZP762B143) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
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No s1 sequence available.
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/clone=lib="762 (synonym: hmel2)"
/tissue_type="metlanoma (MeWo cell line)"
/dev_stage="adult"
/dev_stage="adult"
/lab_host="hH10B"
/note="Vector: pSport1; Site_1: NotI; Site_155 c 148 g 98 t
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/db_xref="taxon:9606"
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5 TR:096029
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                                               mRNA EST 21-APR-2000
1 Homo sapiens cDNA clone IMAGE:2963010 5
096029 7-60. ;, mRNA sequence.
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1 (bases 1 to 526)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian
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Tissue Procurement: ATCC
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/lab_host="DBIOB (phage resistant)"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.

Birectionally cloned into EcoRI/XhoI sites using the place to the place of the plac
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/clone="IMAGE:2963010"
/clone_lib="NIH_MGC_21"
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Pred. No. 4.1e-94;
0; Mismatches 8;
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High quality sequence stop: 591.
Location/Qualifiers
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High quality sequence start: 95
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National Institutes of Health, Mammalian of Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Tel: (301) 496-1550
Tel: (301) 496-1550
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                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone=lib="NIM_SE:3637634"
/clone_lib="NIH_MSC_21"
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Site_2: EcoRI; cDNA made by oligo-dT priming.
Site_2: EcoRI; cDNA made by oligo-dT priming the following of Caloned into EcoRI/XhoI sites using the following of Gadaptor: GGCACAGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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                                                                                                                                                                                                                                                                                                                                                                   Email: Robert Strausberg@nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.lini.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washingtion Genome Center. Vector
Trimming: cross_match from University of Washingtion Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:
http://www.genome.washington.edu
Plate: LLCM6 row: H column: 17
High quality sequence stop: 470.
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NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Other_ESTs: 2821312.3prime
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/note-*Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGS:2821312"
/clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
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                                                                                                                                                                   /lab_host="DH10B (phage-resistant)"
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Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D
Tel: (301) 496-1550
                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 551)

NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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similar to
Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (Dases 1 to 493) NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/. National Institutes of Health, Mammalian Gene Collec
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/clone_lib="NIH_MGC_20"
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/lab_host="Ph10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: xhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5;
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1188 gaagctggagctgagccggcggggagcagccgcccacagggcccacaggccctcagagtgcctc 1247
                                                                                                                                                                                                                                                                                                                                               1428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAAGCTGGAGCTGAGCCGGCGGGAGCAGCCCGCCACAGAGCCAGGCCCTCAGAGTGCCTC 60
                                                                     tggggacagtgctgcggttggccagttggtggtgcccagacctttggccctttgccgggtcccc 1487
                                                                                                                                                                                                                                                                                                                                                                                                       A-AGGTGGAGAAGATCGCTCTGAATTTGGAGGGGTGTGCCCTCAGCCAGGCCAGCCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agaggtggagaagatcgctctgaatttggaggggtgtgccctcagccagggcagcctcag 1307
                 cccggcaggacct 1680
                                                                                                                                                                                                                                                 tgccccatcggggcaccccaaggctggacacagtgagaacggggttgaggaggacacaga 1547
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACGGGGACCCAGGAAGTGGGCCGGTCAGGACCCTGGGGAGGCAGTGCAGCCCTGCCGCCA 179
                                                                                                                                                                                                                                                                                                                                                                                     ACCCCTGGGAGCCAGGGTGGCCGACAAGGTGAGGAAGCGGAGGAAGGTGGATGAAGGTGC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                483;
                                                                                                                                                                                                                             TGCCCCATCGGGGCACCCCAAGGCTGGACACAGTGAGAACGGGGTTGAGTAGGACACAGA
                                                                                                                                                                                                                                                                                                         TGGGGACAGTGCTGCGGTGGCCAGTGGTGGTGCCCAGACCTTGGCCCTTGCCGGGTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Washington University Genome Sequencing Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/iresources.shtml Seq primer: -40Rp from Gibco High quality sequence stop: 423.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Other_ESTs: ba97e12.x1
Contact: Robert Straus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: Robert_Strausberg@nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: (301) 496-1550 
Email: Robert_Straus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NIH_MGC_14"
/clone_lib="NIH_MGC_14"
/tissue_type="renal cell adenocarcinoma"
/lab_nost="DH108 (phage-resistant)"
/lab_nost="DH108 (phage-resistant)"
/note="Organ: kidney; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GCCACGAG(G). Size-selected >500bp for average
insert size 1.8%b. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
03 a 150 c 186 g 53 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 467.2; DB 35; Length 493;
Pred. No. 8.2e-85;
0; Mismatches 9; Indels 1;
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SOURCE
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Best Local Similarity
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                                                                                                                                                                                                          1938 cgagagcccatcggagaccccaggccccgcccggcaggacctgcaggggacgagccagc 1997
2058 caaggcggggggaggcagcagagttgcaggacgcagaggtggagtcttctgccaagtcttgg 2117
                                                                                                                                                                                  550
                                                                                 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: Robert_Strausberg@nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washingtion Genome Center
Trimming: cross_match from University of Washingtion Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:
http://www.genome.washington.edu Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
                                                                         cgagagcccatcggagaccccaggcccagcccggcaggacctacaagggatgagccagc 2057
                                                                                                                                                                                  CGAGAGCCCATCGGAGACCCAGGGCCCCCGCCCGGCAGGACCTGCAGGGGACGAGCCAGC 491
                                                                                                                                                                                                                                                                                      467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Other_ESTs: 2821312.5prime
Contact: Robert Strausberg,
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polyadenylated.
Plate: LLCM6 row: H column: 17
High quality sequence stop: 430.
Location/Qualifiers
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NIH-MGC http://www.ncb1.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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2821312.3prime
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                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DHIOB (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRX/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 173 c 174 g 105 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:2821312"
/clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
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                                                                                                                                                                                                                                                                                                           19.3%;
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                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                         Score 465.8; DB 2
Pred. No. 1.6e-84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: (301) 496-1550

Email: Robert_Strausberg@nlh.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboration

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM293 row: g column: 08

High quality sequence start: 44

High quality sequence stop: 522.

Location/Qualifiers
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1 (bases 1 to 529)

NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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/lab_host="Phil08 (phage-resistant)"
/note="Organ: lymph; Vector: poTB7; Site_1: XhoI; Site_2:
/no
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452; DB 35;
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                                                         CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.fuller: LLCM317 row: e column: 21 High quality sequence start: 2 High quality sequence stop: 532. Location/Qualifiers
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1 (bases 1 to 1296)

NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Tel: (301) 496-1550
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601299883F1 NIH_MGC_21
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/lab_host="NH108 (phage resistant)"
/lab_host="NH108 (phage resistant)"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
Directionally cloned into EcoRI/XhoI sites using the
following 5 adaptor: GGACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
a 416 c 389 g 164 t
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JOURNAL COMMENT
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BE391750
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AUTHORS
TITLE
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ORGANISM
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Best Local Similarity
Matches 577; Conserv
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cyactccacctgggaggaggacgaggaggatgcggaggacgcgggaggacgaggactgcga 110
                                                                          GGCGAGCCACGAGGGACATGTGTACGGTATCGGCACAACTATCCGGATTCTGGTGGAACG
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                                                                                                                                                     GGAGCCGCGGGCGGACGCGTCCCATCTCGTTCCAGTCCAGAATGACAGGGTCCAGAAACT
                                                                                                                                                                                                                              Tissue Procurement: ATCC CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 757)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM252 row: f column: 03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: uterus; vector: pOTB7; Site_1: xhoI; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." a 204 c 251 g 131 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:3604994"
/clone=1b="NHI_MGC_44"
/clone_1b="NHI_MGC_44"
/tissue_type="endometrium, adenocarcinoma cell line"
/tassue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
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. clone IMAGE:3604994 5',
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              405 tg-aggacaatcactcctacatccagtggctgtttcctctgcgagaaccaggagtgaact 463
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Search completed: October 12, 2000, 12:02:37 Job time: 24145 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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57.2	57.2	58.4	58.4	60	60.2	60.2	61.8	62.6	62.6	248.8	251.8	Score	
3.6	3.6	3.6	3.6	3.7	3.8	3.8	3.9	3.9	3.9	15.5	15.7	Query Match	ф
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Anti-sense strand	Nucleotide sequenc	Partial mouse WRN	Mouse histone H2B	HSV-2 strain SB5 C	KSHV long unique c	KSHV LUR DNA (nucl	DNA encoding Pseud	PCR primer for 5'	Randomising oligon	Prostate cancer as	EST clone BK517.	Description	

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Nicotianamine amin		Human PKD1 locus b		Human PKD1 gene.	Human Trk oncogene	Human c-trk oncoge	Human telomerase p	Homo sapiens ambig	Amycolatopsis medi	Human gene express	an LOBO ho	Rat Muncl3-1 encod		adenosine		Human lung tumour	CENP-B cDNA. Homo	Human colon cancer	cDNA encoding a pr	2	Gene encoding a su	Partial mouse WRN	nsert stabi	Human telomerase p	Homo sapiens mamma	Epstein Barr Virus	Nucleotide sequenc	Plasmid pCisEBON f	Plasmid pCisEBON f	Nucleotide sequenc	רסי	Vector pShuttle DN

ALIGNMENTS

V90541 V90541; V90541 standard; cDNA; 375 BP

EST clone BK517. 15-FEB-1999 (first entry)

Human; secreted protein; expressed sequence tag; EST; haematopoiesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic; receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumou gene therapy; ss.

Homo sapiens

10-APR-1998; W09845436-A2 15-OCT-1998. 98WO-US06955

Agostino MJ, Jacobs K, Racie LA, Spaulding V, Lavallie ER, Treacy M; мссоу лм, Merberg 'n

(GEMY) GENETICS INST INC.

10-APR-1997;

97US-0838821

WPI; 1999-070077/06.

New polynucleotides encoding human secreted proteins - derived e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries. from

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RESULT
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Matches 253
                     22-JUN-1998;
17-JUL-1997;
10-OCT-1997;
10-OCT-1997;
10-OCT-1997;
                                                                                                                                                                                                                 Cancer associated antigen; diagnosis; research; treatment; breast cancer; colon cancer; gastric cancer; renal cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a human expressed sequence tag (EST). The polynucleotide, which is a secreted EST, and the encoded protein are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haemastopolesis regulating activity, tissue growth activity, haemastopolesis regulating chemotactic/chemokinetic activity, hemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The polynucleotide may also be useful for gene therapy.
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         98US-0102322.
97US-0896164.
97US-0061599.
97US-0061765.
97US-0948705.
97GB-0021697.
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Pred. No. 4.4e-38;
0; Mismatches 2;
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The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and the name cancer and cancer.
   Sequence 802
                                                                                                                                                                                                                                                                                                        New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                               Chen Y, Gout I, Pfreundschuh M,
                                                                                                                                                                                                                                                                                Claim
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                                  cancer.
                                                                                                                                                                                                                                                                                67;
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 ВP;
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7 other;
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                                                                Randomising
                                                                                   08-JUN-1992
                                                                                                                        Q21833
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                                                                                                      Q21833;
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                                                                                                                                                                                                                                                                                                                   GTCCTCCTGTCCCTGCTGCAGGGGCTGGGGGCTCCCGGAGCTGCTGCGGGCTCCCCTCAGG
                                                                                                                                                                                                                                                                                                                              990ctcctgttccctgctgcaggggctggggcctccggagctgctgcggggctcccctcagg 1406
                                                                                                                                                                                                        CTGGCTGTGTCTTCCCCACCCAGCTNTCCCCTGCGCCCCTGTCTTTGTAAATTGACCCTT
                                                                                                                                                                                                                                            GCAGCCACCAGAAGCCGCGAGGCCCTCAGGGAAGCCCAAGGCCTGCAGAAGCCTCCTGGC
                                                                                                                                                                                                                                                                                CTNTGCTTCGTGACCCGTGACCCATGACCCACAGTGCTGGCCTCCTGTGGGGGCCACTATA
                                     binding;
                                                                                                                        standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                              polypeptide
                                                                oligonucleotide used in
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                                                                                  (first entry)
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                                              evolution
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                                             уd
                                             reverse
                                                               SPERT mRNA prepn.
                                              translation;
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                                                                                                                                                                                                                                                                                                                                                                           Length
                                             SPERT
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Best Local S
Matches 92
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                                                                                                                               Systematic specific; i
                                                                                                                                                                                                                   Q36859;
                                                                                                                                                                                                                                           Q36859 standard;
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             01-AUG-1991;
                                                                                                                                                                   PCR primer for 5' fixed sequence contg. T7 promoter and RBS
                                                                                                                                                                                           22-JUN-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptide(s)
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                                    31-JAN-1992;
                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 390 BP; 125 A; 126 C; 133 G; 6 T; 0 other;
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92; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page
                                                                                                                              c peptide evolution by reverse translation; SPERT; ligand;
inhibitors; probes; assay; cell sorting; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55; 102pp; English.
             91US-0739055
                                    92WO-US00801
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Pred. No. 0.0019;
0; Mismatches 4
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mice which are the fi progeny of a cross of NZB and NZW parents (Portanova et al., J. Immunol. 1144, 4633, 1990). The known epitope consists of ca. 10 amino acids at the N-terminus of the histone HZB protein. To make mRNA encoding candidate polypeptides a 5 fixed sequence composed of a T7 promoter sequence and a ribosome binding site which is recognised by both prokaryotic and eukaryotic ribosomes, terminating in a restriction endonuclease site is synthesised and cloned using a number of oligonucleotides (example shown). A 3 fixed sequence is placed into a restriction site to provide an mRNA encoding the C-terminal trailer sequence of ca. 100 nucleotides lacking stop codons. In addition, a 3 primer annealing site is provided so that cDNA synthesis can be accomplished on the mRNA recovered from partitioned ribosome complexes. See also Q38845-63.
            Sg
                                                 misc_feature
                                                                                       misc_feature
                                                                                                                             Pseudorabies virus.
                                                                                                                                                     Pseudorabies virus; PRV; LLV; large latency transcript; attenuated virus; vaccine; early protein 0; EPO; HSV-1 ICPO; protecting animals; deletion mutants; swine; ds.
                                                                                                                                                                                                       DNA encoding
                                                                                                                                                                                                                                    15-MAY-1995
                                                                                                                                                                                                                                                                                     Q73500 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 390 BP; 125 A; 126 C; 133 G; 6 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                       Pseudorabies virus large latency transcript.
                                                                                                                                                                                                                                 (first entry)
  /*tag= b
/note= "derived f
622..6498
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/note= "derived :
7014..8425
                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                       DNA;
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                                                                                                                                                                                                                                                                                                                             CC Q73500 shows the Pseudorables virus (PRV) large latency transcript CLLT). The basic sequence is derived from PRV strain InFh and PRV CC strain Ka. The LLT overlaps and is transcribed in the opposite CC orientation with respect to the EPO (early polypeptide 0) and the CC immediately early gene (IE180). EPO is nonessential for replicatio, CC LLT is the only gene expressed during PRV latency, and the IE180 CC gene is absolutely necessary for PRV replication. However there are CC 2 copies of IE180 in the genome. It is expected that PRV lacking one CC of the IE180 copies is viable. Deletions in the non-overlapping CC regions of these 3 genes will generate single deletion routants, CC while deletions in overlapping regions will generate double deletion CC mutants. The invention is concerned with the construction of attenuated CC viruses which have a reduced ability to reactivate from latency. This CC can be achieved by functionally disabling the expression of the EPO CC gene, or by disrupting the synthesis of the LLT, or both. (See also CC Q73501 and R60620-24)
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 87; Conserv
V73805;
                                                                                            5716
                                                                                                                                                 5656
                                                                                                                                                                                                      5596
                           V73805 standard;
                                                                                                                                                                                                                                                                                                                         Sequence 8438 BP; 1141 A; 2916 C; 3327 G; 1054 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Column 15-30; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New pseudorables virus mutants for use in vaccine - ha deletion and/or insertion in the early protein O gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cheung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-SEP-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              latency transcript gene
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ilarity 67.4%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "encodes predicted amino acid sequence of ORF2"
                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                     Score 61.8; DB 1
Pred. No. 0.0034;
0; Mismatches 4
                                                                                                                                                                                                                                                                                 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 32207 BP; 7229 A; 9156 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kaposi's sarcoma-associated herpes virus di:hydro:folate reductase and is useful f or diagnosis of Kaposi's sarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sarcoma in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Column 155-182; 109pp; English.
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                                                                                                                       Bohenzky RA,
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25-JUL-1996;
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25-JUL-1996;
25-JUL-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KSHY; HHY08; human herpes virus 8; macrophage inflammatory protein II; interleukin-6; II-6; interferon regulatory factor; rheumatoid arthritis; complement-binding protein; glycoprotein; capsid protein IV; infection; immediate early protein; Kaposi's sarcoma; protective vaccine; lymphoma;
                                                          22-JUL-1997;
                                                                          05-FEB-1998
                                                                                        WO9804576-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KSHV long unique coding region
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       96US-0757669.
96US-0686243.
96US-0686349.
96US-0686350.
96US-0687253.
                                                          97WO-US13346
                                                                                                                      /product= capsid protein IV
complement (123808..127296)
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complement (111931..112443)
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complement (58976..60175)
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complement (17261..17875)
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complement (88410..88910)
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28661..29
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Conservative

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Score 60.2; DB 19; Pred. No. 0.0082; 0; Mismatches 78;

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AGGATGACGAGGAGGATGACGAGGAGGATGACGAGGATGACGAGGATGACGAGG 126210

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the Kaposi's sarcoma-associated herpes virus (KSHY). KSHY is also known as human herpes virus 8 (HHV8). This sequence contains the DNAs of the Ci invention which encode KSHY polypeptides selected from: (a) viral CC macrophage inflammatory protein (MIP) II: (b) viral interleukin-6; (C) viral IRF 1; (d) complement-binding protein; glycoproteins B, M or L; (d) capsid protein IV encoded by ORF65; and (e) immediate early protein CC encoded by ORF63. Labelled probes for the nucleic acid, proteins encoded by Lt, and antibodies (Ab) specific for the proteins are useful for CC detecting HHV8, specifically for diagnosis of Kaposi's sarcoma, in body CC fluids or tissue samples. HHV8 infections can be treated with antisense CC or triplex forming molecules or agents that bind specifically to the protein. Ab may be used for prophylaxis or treatment of HHV8 infection, while the protein can be used in protective vaccines. Ab may also be used CC office that by the protective vaccines. Ab may also be used CC office that pumphomas, and HHV8 may be implicated in many other lymphomas, and HHV8 may be implicated in many consistency of a patient of cells and animals containing the CC used as targets for antiviral drugs, e.g. dihydrofolate reductase gene can be inhibited with methotrexate. These can also be used to determine CC the immune status of a patient infected with HIV. HHV8 derived protein CC used in the containing the used as an anti-inflammatory agent for, core, treating rheumatoid arthritis. This sequence is stated as containing CC on the protein can be used as an anti-inflammatory agent for, containing the cont
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13-NOV-1996;
13-NOV-1996;
Sequence 137507 BP; 32579 A; 37795 C;
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/product- "ORF#9b protein" /note- "encoded protein shown in W72222" complement (1190514520)	# ct_	/"cay-"" /product= "ORF#7 protein" /note= "encoded protein shown in W72175" /omplement (960411855) /*tag= n	92,11.0	<pre>"rag" k /product "ORP#6b protein" /note= "encoded protein shown in W72245" 6446. 8482</pre>	/*tag= j /product= "ORF#6c protein" /note= "encoded protein shown in W72246" 63268482	/*tag= 1 /*tag= 1 /product= "ORF#6d protein" /note= "encoded protein shown in W72247" 62968482	<pre>/*tag= h /product= "ORF#6e protein" /note= "encoded protein shown in W72248" 6167 8487</pre>	/*tag = 0 /*tag = 0 /product = "ORF#6f protein" /note	<pre>/*tag= f /product= "ORF#6g protein" /note= "encoded protein shown in W72250" . 6026</pre>	/*tag= e /product= "ORF#5 protein" /note= "encoded protein shown in W72174" 60178482	<pre>/*tag= d /product= "ORF#4 protein" /note= "encoded protein shown in W72173" complement (38026447)</pre>	<pre>/*tag= c /product= "ORF#3 protein" /product= "ORF#3 protein shown in W72172" complement (31303735)</pre>	<pre>/*tag= b /product= "ORF#2 protein" /note= "encoded protein shown in W72171" 22292930</pre>	tag- rodu ote- 70.	L)	virus type 2.	in SB5; immunological response induction; therapy;
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/product- "ORF#33 protein"
/note- "encoded protein shown
complement (58060..58977)
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/0216..41973
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/note= "encoded protein shown
61241..62071
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/note= "encoded protein shown
60759..61151
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/note= "encoded protein shown
54393..58115
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/note= "encoded protein shown
complement (47305..49662)
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/product= "ORF#27 protein"
/note= "encoded protein shown in W72192"
complement (44853..47297)
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/note= "encoded protein shown
complement (51701..53575)
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/note= "encoded protein shown
complement (50035..51666)
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/product= "ORF#26 protein"
/note= "encoded protein shown
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Best Local S
Matches 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JAN-1992;
02-AUG-1990;
01-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   V64950-V64972 are sequences used in a method polypeptide ligand of a target molecule. The be used in assays, in diagnostic procedures, inhibitors of target molecule function, as pragents, or may have catalytic activity.
                                                                                                                                         )7/c
X83007 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Production of polypeptide ligands using mRNA-polypeptide coby affinity selection, RNA amplification and polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ligand; assay; sequestering a
                                     Mouse; WRN; Werner's syndrome; detection; diagnosis; autosomal;
                                                                                         31-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gold L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5843701-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
Mus musculus.
                         recessive disorder;
                                                                 Partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-044575/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 10; Column 45-46; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NEXS-)
                                                                                                                                                                                                         125
                                                                                                                                                                                                                       153 cgaggacgaggagtcggagg 172
                                                                                                                                                                                                                                                           65
                                                                                                                                                                                                                                                                                   93
                                                                                                                                                                                                                                                                                                                                       33
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                                                                                                                                                                                                                                                                                                                           ggaggacgaggactgcgaggacgcgaggccgccggcgagggacgcaggggacgcagggga
                                                                                                                                                                                                        cgacgccatggttgcgatgg
                                                                                                                                                                                                                                                                                                           histone
                                                                                                                                                                                                                                                                                                                                                             l Similarity
89; Conserv
                                                              mouse WRN genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEXSTAR PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pribnow D,
                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                        (first
                                                                                                                                                                                                                                                                                                                                                                                                                              BP; 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92US-0829461.
90US-0561968.
91US-0739055.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnostic; inhibitor; probe; cell sorting; catalysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9205-0829461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                         3.68;
                         phenotype;
                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                              A; 46 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith
                                                                                                                                          51259
                                                                                                                                                                                                         144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                epitope oligonucleotide fragment
                                                                                                                                                                                                                                                                                                                                                             ; Score 58.4; D; Pred. No. 0.01 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'n,
                                                                                                                                          ВP
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                                                                                                                                                                                                                                                                                                                                                                         58.4;
No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                              1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as probes,
                                                                                                                                                                                                                                                                                                                                                                       .01;
                                                                                                                                                                                                                                                                                                                                                                51
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                                                                                                                                                                                                                                                                                                                                                                                       20;
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                                                                                                                                                                                                                                                                                                                                                                                       Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sorting, as
sequestering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conjugates
de synthesis
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                 Fusion protein; stabilising polypeptide; proteolytic degradation; resistance; half-life; autoimmune disease; inflammation; nitro drug; IkappaB regulator protein; inflammatory bowel disease; in vivo imaging;
                                                 Epstein-barr virus
                                                                            nitroreductase protein; enzyme therapy;
                                                                                                                         Nucleotide sequence of the stabilising sequence-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-APR-1996;
29-DEC-1995;
29-DEC-1995;
30-JAN-1996;
30-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a fragment of the genomic sequence containing the coding region for the mouse WRN gene (M83004). The corresponding human gene (M8301) encodes a protein related to Werner's syndrome. The products can be used for the detection and treatment of Werner's syndrome (MS), an autosomal recessive disorder with a complex phenotype
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 7; 153pp;
                                                                                                                                                                                                                                                                                                                                                                                                                              as well as related diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-363671/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DARW-)
(OSHI/)
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                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                             actgcgactccacctgggaggaggacgaggaggatgcggaggacgaggact 106
                                                                                                                                                                                                                                                                           AGGAGGAGCAGGAGGAG
                                                                                                                                                                                                                                                       cggaggagccgcgggcggcg
                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mulligan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DARWIN
                                                                   pathological
                                                                                                                                                                                                                                                                                                                                                        Similarity 63.0
89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        51259 BP; 14533 A; 9635 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid molecule encoding the WRN gene product
or detection and treatment of Werner's syndrome, and
                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96US-0632175.
95US-0009409.
95US-0580539.
96US-0010835.
96US-0594242.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-US20785
                                                                                                                                                                                       DNA;
                                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oshima J,
                                                                                                                                                                                                                                                                                                                                                                 3.6%;
                                                                                                                                                                                       799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                                                                       ВP
                                                                                                                                                                                                                                       140
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                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                      Score 58.4; DI Pred. No. 0.01: 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schellenberg
                                                                                                                                                                                                                                                                                                                                                                                                        10266 G; 16825 T; 0 other;
                                                                            prodrug
                                                                                                                                                                                                                                                                                                                                                                 .016;
                                                                                                                                                                                                                                                                                                                                                                           DB 18;
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                                                                           protease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and related
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28-MAY-1998 W09822577-A1

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                                                                                                                                                                                                                                                                                                                                                                                                                       CC This is a nucleotide sequence of the stabilising sequence-encoding CC insert. The invention provides a method for increasing the resistance of a core protein to proteolytic degradation that comprises linking or CC inserting onto or into the core protein a stabilising polypeptide of CC formula [(Glya)X(Glyb)Y(Glyc)Z]n where Glya, Glyb, Glyc are 1-6 CC sequential Gly residues and X, Y, Z are Ala, Ser, Val, Ile, Leu, Met, CC Phe, Pro or Thr and n can be anything between 1-65, X, Y and Z need not CC encoding the stabilising polypeptide can be linked onto or inserted into CC a nucleic acid encoding a core protein. The fusion proteins of the CC invention are more resistant to degradation by proteases and, thus, have CC a longer half-life than the unfused core protein. The products can be used for treating autoimnume diseases, cancer and inflammation. In CC particular, the core protein may be an IkappaB regulator protein for the treatment of inflammatory bowel disease, or a nitroreductase protein CC which can activate nitro drugs in enzyme/prodrug therapy to treat cancer or other pathological conditions. The fusion proteins can also be used in vivo imaging.
                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                 1018
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                            306
                                                                                       958
                                                                                                                  246
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                                                                                                                                                                                                                                                   778
                                                                                                                                                                                                                                                                                                         718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-312463/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JUN-1997;
15-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MASU/)
                                                                                                                                                                                                                                                                              66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide sequence containing glycine
                                                                                                                                                                                                                                                                                      aaggtggaggaaggaagcccggggaccccgaccacgaggccagcacccagggtcgg
                                                                                                           caagacaagctgcggaggttcaagcccagctctctgccgcatccgctcgagggctccagg
                                                                                                                                                                                         cagctggtgcacttcgcctgggagcacttccggcccgctgcaagttcgtctgggggccc
                                                                                                                                                                                                                                                                      gtgcggcagagtgccctggactacttcatgttcgccgtgcgctgccgacaccagcgccgc 837
                                                                                                                                                                                                                                                                                                                                  272;
                                                                                                                                                                                                                                                                                                                               Similarity 43.;
72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MASUCCI
                                                                                                                                                                                                                                                                                                                                                                                                   799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteins resistant to proteolytic degradation a core protein with a stabilising polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                   ВP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0048945
96US-0030986
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                                                                                                                                                                                                                                                                                                                                                                                                  201 A; 106 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120pp;
                                                                                                                                                                                                                                                                                                                                            3.6%;
                                                                                                                                                                                                                                                                                                                              Pred. No. 0.02
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                                                  479 G;
                                                                                                                                                                                                                                                                                                                                                                                                13 T; 0 other;
                                                                                                                                                                                                                                                                                                                                            .02;
                                                                                                                                                                                                                                                                                                                               358;
                                                                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                         799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comprising
                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                              Gaps
                              1077
                                                                                   1017
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                                                                                                                                       957
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RESULT 1
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      The present sequence is an anti-sense strand of commercially available plasmid pcMYEBNA from which Epstein Barr Virus Nuclear Antigen 1 (EBNA 1) encoding DNA is obtained. EBNA 1 protein is used to stably maintain episomes containing EBV origin of replication (orif) and a gene encoding protein or RNA of interest. Eucaryotic host cells expressing EBNA 1 protein are transfected with these episomes to produce recombinant cell lines expressing multiple genes of interest. This provides a rapid and reliable method of stably expressing multiple genes in transfected cells. The episomes are useful in the transfection of genes encoding receptors, transporter proteins, ion channels, adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-sense strand; plasmid pCMVEBNA; EBNA 1; episome; transfection; Epstein Barr Virus Nuclear Antigen 1; origin of replication; EBV orip; eucaryotic host cell; recombinant cell line; ion channel; multiple gene expression; receptor; transporter protein; gene therapy; transcription factor; adhesion molecule; antisense therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1318
                                                                                                                                                                         New method useful for
                                                                                                                                                                                                             WPI; 1999-610610/52
                                                                                                                                                                                                                                                                                      18-MAR-1998;
06-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-sense strand of pCMVEBNA plasmid.
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                                                                                                                                                                                                                                                                                                                            12-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                    23-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                            WO9947647-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Epstein-barr virus
                                                                                                                                                Example 1; Fig 1; 86pp;
                                                                                                                                                                                                                                                               (PHAR-) PHARMACOPEIA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       caggagcaggagggcaggagggcaggag 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aagatcgctctgaatttggagggtgtgccctcagccagggcagcctcaggacggggacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ctgagccggcgggagcagccgcccacagagccaggccctcagagtgcctcagaggtggag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for expressing genes gene therapy -
                                                                                                                                                                                                                                      Horlick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
transcription
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                                                                                                                                                                                                                                                                                      98US-0040961.
98US-0130114.
                                                                                                                                                                                                                                                                                                                            99WO-US03307
                                                                                                                                                                                                                                                                                                                                                                                                                                        complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA;
                                                                                                                                                                                                                                      RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell immortalisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5452
                                                                                                                                                 English.
                                                                                                                                                                                                                                      Robbins
                                                                                                                                                                                                                                                                                                                                                                                                                                        (3032..4957)
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                                                                                                                                                                                                                                                                                                                                                                                                              protein"
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                                                                                                                                                                                                                                                                                                                                                                                                     Virus Nuclear
                                                                                                                                                                                    recombinant eukaryotic
episomes
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desired
                                                                                    encoding
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                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   be used to transfect cells in gene therapy, amplification, cell immortalisation, etc.
                                                                DNA library; identification;
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                                                                                                    (first
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                                                                                                                                          DNA;
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Pred. No. 0.023;
0; Mismatches 358;
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                                                                                                                                                                                        1485
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                                                                multiple cloning site;
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07-OCT-1999 WO9950457-A1 Synthetic

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 16; Page 43-50; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel method for generating an antisense library targeted to a selected RNA transcript. The methods can be used for identifying antisense agents and for identifying target sites for antisense-mediated inhibition of a selected gene. The use of a direct library for target site selection significantly simplifies the screening process, since only very small libraries need be prepared and assayed. This sequence represents the vector pShuttle which is used in the method of the process.
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06-NOV-1998;
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aagatcgctctgaatttggaggggtgtgccctcagccagggcagcctcaggacggggacc
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                                                                                                                                           agcgtggagccccaggatgcgggacccctggagaggagccagggggatgaggcaggggc
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                                                                                                                                                                                                                                                                                        caagacaagctgcggaggttcaagcccagctctctgccgcatccgctcgagggctccagg
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272; Conservative
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for identifying target
of a selected gene -
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98US-0107504
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43.2%;
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No. 0.
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antisense-mediated
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EBV nuclear

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This polynucleotide comprises the DNA sequence of vector plasmid pCMVKmTR-EPI, which contains an Epstein-Barr virus (EBV) origin of replication from plasmid pCEP4, a coding region for EBV nuclei antigen A from pCEP4, a pair of inverted terminal repeats from adeno-associated virus, a cytomegalovirus enhancer/promoter, a
                                                                        Polycationic agents bas
with nucleic acid - to
and protect it against
gene therapy
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Chimeric - 4
Chimeric - 4
Chimeric - 1
                                                       Disclosure; Page 77-80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                     (CHIR ) CHIRON
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                                                                                                                                                                                                                                                                                   terminator
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    Epstein-Barr virus.
    Adeno-associated vi-
Cytomegalovirus.
    Bos taurus.

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                                                                                                                                                                                                                                                                                  /*tag= e
/note= "CMV
6818..7050
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/product= "
2623..4559
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/note= "EBV origin
4928..5104
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                                                                            based on alpha-amino acids, able to complex to facilitate its entry into cell, condense it not serum degradation, particularly for use in
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te= "AAV
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nic agent; ss.
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Best Local
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                                                                                                                                                                                                                                                                                                       1097
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                                     Z22248 standard;
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                                     DNA;
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Matches 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Examples; Fig 3A-J; 64pp; English.
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A1590782 tw25d09.x
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BE409569 601299338
BE399750 6012893311
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AI816189 au45h07 x
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AI816230 au45h07 y
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AI115047 u141f12 y
BE274933 6011231408
AI1172669 u992f06 y
BE394864 601231409
AW1625673 19380 MAR
AW762644 ur64h02 y
BE482073 167730 BA
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밁 KEYWORDS SOURCE ORGANISM ACCESSION VERSION Query Match Best Local 361 Mar. Local St. 681; 524 aggagcggcttgtccgggcctacgagctcatgctggggcttctacggggatccggctggagg TCGTCTGGGGGCCCCAAGACAAGCTGCGGAGGTTCAAGCCCCAGCTCTCTGCCGCATCCGC 999agctgccgggggtgcggcagagtgccctggactacttcatgttcgccgtgcgctgcc tcgagggctccaggaaggtggaggaaggaagccccggggacccccgaccacgaggcca 1003 GACACCAGCGCCGCCAGCTGGCACTTCGCCTGGGAGCACTTCCGGCCCCGCTGCAAGT gacaccagcgccgccagctggtgcacttcgcctgggagcacttccggccccgctgcaagt gcctcgagcacttccaggcgccactggtccgcttcttcctggaggagacgctggtgcggc accgaggcacgggcacggtgggccgagcacagaactaccagaagcgcttccagaacctga 643 tcgtctgggggccccaagacaagctgcggaggttcaagcccagctctctgccgcatccgc GCCTCGAGCACTTCCAGGCGCCACTGGTCCGCTTCTTCCTGGAGGAGACGCTGGTGCGGC actggcgcagccaccaccacctccgcatcacacgcatcctcaagtcgccgtgtgagctga ACCGAGGCACGGCACGGTGGGCCGAGCACAGAACTACCAGAAGCGCTTCCAGAACCTGA GGGAGCTGCCGGGGGTGCCGAGAGTGCCCTGGACTACTTCATGTTCGCCGTGCGCTGCC ACTGGCGCAGCCACAACAACCTCCGCATCACACGCATCCTCAAGTCGCTGGGTGAGCTAG AGGAGCGGCTTGTCCGGGCCTACGAGCTCATGCTGGGCTTCTACGGGATCCGGCTGGAGG Eukaryota; Metazoa; Chordata; Craniata; Verteb Mammalla; Eutherla; Primates; Catarrhini; Homi 1 (bases 1 to 729)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Teli (301) 496-1550 Email: Robert_Strausberg@nih.gov Plate: LLCM219 row: f column: High quality sequence stop: 627. Homo sapiens EST mRNA sequence. BE264806 BE264806.1 GI:9138366 Similarity 151 Conservative /lab_host="DHIOB (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; CDNA made by oligo-dT priming. Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

218 c 268 g 92 t /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:353657"
/clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cstl_line="MGC3" Location/Qualifiers 39.8%; Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo. Score 636.6; Pred. No. 3.1e 0; Mismatches 0; ; DB 34; 3.1e-121; has 19; 18 Indels Length 729; Collection (MGC) ω •• Gaps 420 943 360 883 763 180 703 300 823 240 60 583

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   gatgaggcagggggccacggggaagataggcccggagcccttaagcccccaaagagagcaag
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.
Plate: LLCM97 row: h column: 23
High quality sequence stop: 742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D Tel: (301) 496-1550
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NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection
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                                                     Conservative
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/Clone_lib="NIH_MCC_20"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
cloned into ECORI/XhoI sites using the following 5'
adaptor: GCCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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/db_xref="taxon:9606"
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                                                                   37.3%;
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CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM286 row: 1 column: 17
High quality sequence start: 86
High quality sequence stop: 727.
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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Tissue Procurement: ATCC/DCTD/DT
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/lab_host="Dul08 (phage-resistant)"
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/db_xref="taxon:9606"
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                  cgaggagtcggaggagccgcgggcgcgggcccagctcgttccagtccagaatgacagg
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CGAGGAGTCGGAGGAGCCGCGGCGCGCGCCCAGCTCCTTCCAGTCCAGAATGACAGG
                                                                 GAGCACAGAACTACCAGAAGCGCTTCCAGAACCTGAACTGGCGCAGC
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov plate: LLCM288 row: j column: 11
High quality sequence start: 20
High quality sequence stop: 663.
Location/Qualifiers
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Tissue Procurement: ATCC/DCTD/DTP
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601278145F1 NIH_MGC_20
                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
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NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: xhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5;
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Bezkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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/db_xref="taxon:9606"
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Pred. No. 8e-111;
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1 (Dases 1 to 522)
Koehrer, K., Beyer, A., A
EST (Koehrer, et al.)
Unpublished (1999)
                                                                                                                                            Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Canc. Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by BMFZ (Biomedical Research Center at the Charite, Berlin/Germany) within the cDNA sequencing consortium of the Genome By-10-14-15.
                                                                                                                                                                                                                                                                                                                                                                                                AL120919 522 bp mRNA
DKFZp762B143_r1 762 (synonym: h
DKFZp762B143 5', mRNA sequence
AL120919
                                                                 No s1 sequence available.
This clone (DKFZp762B143) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14(
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp762B143"
/clone_lib="762 (synonym
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Primates;
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium ()
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
                                                                                                                                                                                                                   BE410591.1
EST.
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601303311F1 NIH_MGC_.
                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 591)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collect
                                                                                                                                                                                                                                                         mRNA sequence.
                                                                                                                                                                                         Homo sapiens
                                                                                                           Unpublished (1999)
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/dev_stage="adult"
./lab_host="bHIDB"
/note="Vector: pSport1; ;
a 155 c 148 g 9)
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mRNA sequence.
BE398108
BE398108.1 GI:
EST.
                                                BE398108 529 bp mRNA
601290328F1 NIH_MGC_8 Homo sapiens
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plate: LLCM37 row: f column: 03
High quality sequence start: 95
High quality sequence stop: 591.
Location/Qualifiers
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//lab_host="DBHUB (phage resistant)"
/note="organ: phacenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5; adaptor: GGCAGGAGG(5). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 149 C 196 g 109 t 1 others
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/clone_lib="NIH_MGC_21"
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/db_xref="taxon:9606"
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Pred. No. 2.1e-94;
0; Mismatches 3
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                                                                                                       agccccaggatgcgggacccctggagaggagccagggggatgaggccagggggccacgggg
aagataggccggagcccttaagccccaaagagagcaagaagaggaagctggagctgagcc 1204
                                                                                                                                                                                                   GCCCAGAGCATAGCAAGGGTGGGGGCCA-GGTGGACGAGGGGCCCCCAGCCACGGAGCGTGG
                                                                                                                                                                                                                                      aggaggaaggaagcccggggaccccgaccacgaggccagcacccagggtcggacctgtg 1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agctgcggaggttcaagcccagctctctgccgcatccgctcgaggggctccaggaaggtgg 964
                                                                    AGCCCCAGGATGCGGGACCCCTGGAGAGGAGCCA-GGGGATGAGGCAGGGGGCCACGGGG
                                                                                                                                                                                                                                                                                                                                  AGGAGGAAGCAAGCCCCGGGGACCCCGACCAACGAGGCCAACCCCA-GGTCGGACCTGTG
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NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian G Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
plate: LLCM293 row: g column: 08
High quality sequence start: 44
High quality sequence stop: 522.
Location/Qualifiers
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Homo sapiens
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//db xref="taxon:9606"
//clone="IMAGE:3620767"
//clone_Iib="NIH_MGC_8"
//tissue_type="Burkitt lymphoma"
//lab_host="DH10B (phage-resistant)"
//note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
//note="Organ: lymphoma"
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Pred. No. 1.3e-83;
0; Mismatches 4
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Local Similarity 84.6%;
hes 668; Conservative
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gtgtgagctgagcctcgagcacttccaggcgccactggtccgcttcttcctggaggagac
                                                                                                   cggctggaggaccgaggcacgg-gcacggtgggccgagcacagaactaccagaagcgctt 632
                                                                                                                                          99c99gagcagccgcc
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                                           ccagaacctgaactggcgcagccacaacaacctccgcatcacacgcatcctcaagtcgcc
                                                                                     CGGCTGGAGGACCGACGCGCGCGCACGGTGGGCCCAAGCACAAACTACCAGAAGCGCTT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
BE409569
BE409569.1 GI:9346019
EST.
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601299883F1 NIH_MGC_21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.National Institutes of Health, Mammalian
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1 (bases 1 to 1296)
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                                                                                                                                                                                                                                                                                   /db_xref="taxxn:9606"
/db_xref="taxxn:9606"
/clone="IMAGE:3639948"
/clone="IMAGE:3639948"
/clone=lib="NIH_MGC_21"
/tissue_type="Choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="Directionally cloned into EcoRIXhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
27 a 416 c 389 g 164 t
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                                                                                                                                                                                                   Score 442; DB 35;
Pred. No. 3.4e-81;
0; Mismatches 90;
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IMAGE:3629948
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                                                                                                                                                                                           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergenih.gov
Tissue Procurement: ATCC
                                    CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM252 row: f column: 03
                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I Mammalia; Eutheria; Primates; Catarrhini; Hominidae; I (bases 1 to 757)

NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

National Institutes of Health, Mammalian Gene Collect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE391750 757 bp
601283311F1 NIH_MGC_44
mRNA sequence.
BE391750
High quality sequence start: High quality sequence stop: (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens cDNA clone IMAGE: 3604994
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Best Local Similarity 92.9%;
Matches 577; Conservative
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/db_xref="taxon:9606"
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/clone=lib="NIH_MGC_44"
/clone=lib="NIH_MGC_44"
/clone=lib="NIH_MGC_44"
/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; vector: poTB7; Site_1: xhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
70 a 204 c 251 g 131 t 1 others
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Pred. No. 7.6e-80;
0; Mismatches 31;
       contains element
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     Homo sapiens
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                   cDNA clone
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CTATCCGGATCTGGTGGAACGAGACTGCAATGGGGACACGCCAAACCTGAGTTTCTACAG
              ctatccggatctggtggaacgagactgcaatggggacacgccaaacctgagtttctacag
                                                   aggggacgaggacgaggagtcggaggagccgcggggcgcgcgggcccagctccagtc
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Query Match
Best Local Similarity
Matches 427; Conserv
                           gccgagcatggacgaccccgactgcgactccacctgggaggaggaggacgaggaggatgcgga
GGACGCGGAGGACGACTGCGAGGACGGCGAGGCCGCCGGCGCGAGGGACGCGACGC
                                                                                                     GCCGAGCATGGACGACCCCGGGTGCGACTCCACCTGGGAGGAGGACGAGGAGGATGCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco.
Location/Qualifiers
1, .433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I Tel: 314 286 1810
Fax: 314 286 1810
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Contact: Wilson RK
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Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
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AI459806
AI459806.1 GI:4312687
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                                                                                                                                                                                                                                                                                                                                                                         101
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                           /tissue_type="oligodendroglioma"
/dev_stage="44 years"
/lab_host="SOLR"
/lab_host="SOLR"
/note="Organ: brain; Vector: pBluescript SK- (Stratagene);
Site_1: EcoRI; Site_2: XhoI; Double-stranded cDNA was
prepared from human oligodendroglioma using primer
5'-GAAGAGAGAGAGAGAACTAGATCTGAGT(18)-3'. An EcoRI
adaptor was used on the 5' end of the cDNA as follows:
5'-AATTCGGCACGAC-3'. The library was size-selected and
went through one round of amplification. Average insert
size is 1.7 kb, with a range from 0.4-12 kb. Tumor
identification by consensus pathology; contains
chromosome ip and 19q deletion as determined by CGH. This
library was constructed by Dr. Martin Schiller (Johns
Hopkins University)."
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/db_xref="taxon:9606"
/clone="IMAGE:1955684"
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                                                                                                                                                                                                                                     26.6%;
                                                                                                                                                                                                               0;
                                                                                                                                                                                                          Score 425.8; DB 1
Pred. No. 6.9e-78;
0; Mismatches 2
                                                                                                                                                                                                                                                           DB 10;
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                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                           Length 433;
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124
                                                   146
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REFERENCE
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Other_ESTs: au45h07.yl
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 431.
Location/Qualifiers
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4444 Forest park Parkway, Box 8501, St. I
Tel: 314 286 1800
Fax: 314 286 1810
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AI816189.1 GI:5431735
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                                  73
                       and 3' adaptor sequence:

5'-GAGAGAGACTGCAGTTTTTTTTTTTTTTTT-3'. The library was size-selected for >0.5 kb inserts and has an average insert size estimated at 1.2 kb. This library was constructed using the CAP-trapper method for full-length enrichment and has not undergone amplification. Librar was constructed by Dr. Claudio Schneider (INCIB-Area Science Park, Trieste, Italy). "

143 c 142 g 73 t 1 others
                                                                                                                                                                                                                        /note="Organ: brain; Vector: pBluescript SK (Stratagene); Site_1: Ssti; Site_2: Xhoi; Double-stranded cDNA was prepared from human fetal brain tissue. 5' and 3' adaptors were used in cloning as follows: 5' adaptor
                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TukGE:251757"
/clone_lib="Schneider fetal brain 00004"
                                                                                                                                                                                                                                                                                              /dev_stage="5 months post-conception"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                               /tissue_type="frontal lobe"
                                                                                                                                                                                                                                                                                                                                                   /sex="male"
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AUTHORS
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VERSION
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Query Match

26

Score 423;

DB 13;

Length 432;

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Best Local Similarity
Matches 426; Conserva
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                                                                                             Email: Robert_Strausberg@nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MCC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washingtion Genome Center
Trimming: cross_match from University of Washingtion Genome Center
PHRAP Suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:
http://www.genome.washington.edu
plate: LLCN9 row: E column: 21
High quality sequence stop: 183.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Other_ESTs: 2822396.3prime
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2822396.5prime NIH_MGC_7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
1 (bases 1 to 432)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                            Location/Qualifiers
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          M Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Rodentia; Sciurognathi
1 (bases 1 to 654)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian G
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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BE282484.1
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                                                                                                                                                                                                                                                       house mouse
                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           432
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/clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/lab_host="D10B (phage-resistant)
/lab_host="D10B (phage-resistan
                                                                                                                                                                                                                                                                                                       GI:9158085
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Pred. No. 1.2e-75;
0; Mismatches 5;
                                                                                                                                                                      Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                        cDNA clone
                                                                                                  Gene Collection
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IMAGE:3495186
                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                         Murinae;
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JOURNAL COMMENT REFERENCE AUTHORS TITLE SOURCE ORGANISM

ACCESSION VERSION

KEYWORDS

RESULT 1 BE282484 LOCUS

DEFINITION

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ccagaacctgaactggcgcagcacaaccaacctccgcatcacacgcatcctcaagtcgcc 692
                                                                                    CCAACTTGAGGACCGGAACACAGGCGCGCGTATGCCGTGCACAGAACTTCCAGCCACGCTT
                                                                                                                                                                             CAAGGAAGTCAGAGAGCGTCTTGTCCGGGCCTATGAGCTCATGCTGGGCTTCTATGGGAT
ACACAACCTCAAAAGCCACAGACACAACCATCTGCGTATTACACGCATCCTCAAGTCGCT
                                                                                                           ccggctggaggaccgaggcacgggcacggtgggccgagcacagaactaccagaagcgctt 632
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8545 row: f column: 19
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/strain="CZECH II (feral)"
/db_xref="taxon:10090"
/clone="IMAGE:3495186"
/clone=lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tu
Stem cell origin."
/lab_host="DHIOB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; .Site_2: NotI; Cloned unidirectionally. Primer: Oligo (Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

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atggggacacgccaaacc-tgagtttctacagaaatgagatccgcttcctgcccaacggc
                                                                                                                                                                                               GGGCGGCGCGCCCAGCTTCGTTCCAGTCCAGAATGACAGGGTCCAGAAACTGGCGAGCC
                                                                                                                                   gggcggcgcgggcccagc-tcgttccagtccagaatgacagggtccagaaactggcgagcc 237
                                                                                                                                                                                 AGGCCGCCGGTGCGAGGGACGCGGACGCAGGGACGAGGAGTCGGAGGAGCCGC
                                                                    acgagggacatgtgtaggtatcggcacaac-tatccggatctggtggaacgagac-tgca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov Plate: LLCM257 row: c column: 01 High quality sequence start: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: Robert_Strausberg@nih.gov Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) • Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vo
Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 549)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/
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BE391975
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Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="endometrium, adenocarcinoma cell line"
/tlab_host="DHIOB (phage-resistant)"
/note="Organ: uterus; vector: pOTB7: Site_1: XhoI; Site_2:
PCORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 133 c 184 g 106 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3606840"
/clone_lib="NIH_MGC_44"
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97.7%;
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Washl,NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: estewatson.wustl.edu
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI816230 400 bp mRNA EST 09-JUL-1999 au45h07.yl Schneider fetal brain 00004 Homo sapiens cDNA clong IMAGE:2517757 5' similar to contains element MSR1 repetitive
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Contact: Wilson RK
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMAGE Consortium (info@image.llnl.gov)
Seq primer: -40RP from Gibco
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Fax: 314 286 1810
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        86
5'-GAGAGAGACTCGAGTTTTTTTTTTTTTTTTT-3'. The library we size-selected for >0.5 kb inserts and has an average insert size estimated at 1.2 kb. This library was constructed using the CAP-trapper method for full-length enrichment and has not undergone amplification. Librar was constructed by Dr. Claudio Schneider (LNCIB-Area Science Park, Trieste, Italy). "
                                                                                                                                                                                                                                                                                    /note="Organ: brain; Vector: pBluescript SK (Stratagene);
Site_1: SstI; Site_2: XhoI; Double-stranded cDNA was
prepared from human fetal brain tissue. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
                                                                                                                                                                                                                and 3' adaptor sequence:
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/dev_stage="5 months post-conception"
/lab_host="DH10B"
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/clone_lib="Schneider 1
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/db_xref="taxon:9606"
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Search completed: October 12, 2000, 12:02:56 Job time: 24164 sec

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Gure A, Sahin U,

O'Hare M, Scanlan MJ,

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Tureci O; Pfreundschuh M,

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Claim
                                                                                                                                            New isolated cancer associated nucleic acids and polypeptides isolated using sera from cancer patients, used to develop profor the diagnosis, monitoring or treatment of cancers
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products

The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and

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The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions the invention product as a produc

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Best Local Similarity
Matches 601; Conser
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                                                                   Human; secreted protein; expressed sequence tag; EST; haematopoiesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic; receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumou: gene therapy; ss.
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10-APR-1998;
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                                                                                                                                                                       standard;
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98WO-US06955
                                                                                                                                                                      cDNA;
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Pred. No. 5e-90;
0; Mismatches 20;
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RESULT 4
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ID X53491 standard; DNA; 114955 BE
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AC X53491;
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DT 05-JUL-1999 (first entry)
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DT 05-Jul-1999 (first entry)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a human expressed sequence tag (EST). The polynucleotide, which is a secreted EST, and the encoded protein are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopolesis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, activin/inhibin activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The polynucleotide may also be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides encoding human secreted proteins e.g. human blood, kidney, foetal lung, placenta, test ovary, pituitary, retina and colon cDNA libraries.
                                                                                                                                                                                                                                                                 2347
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   Antisense oligonucleotide; multiple target; antisense impaired respiration; inflammation; lung disease;
                                                   Human adenosine Al receptor antisense oligonucleotide
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Racie LA, Spaulding
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Pred. No. 4.9e-46;
0; Mismatches 1;
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The specification describes antisense oligonucleotides (X52869-X55271) CC directed against at least 2 mRNAs selected from target genes, coding and connecting regions of RNAs corresponding to target genes, gene cointitation codons, genomic flanking regions, intron-exon borders, the confidence of the juxta-section between coding and non-coding cregions and all segments of RNAs encoding proteins associated with one cor more diseases, conditions or mixtures. The antisense oligonucleotides cor more diseases, conditions or mixtures. The antisense oligonucleotides cor more diseases, conditions or mixtures. The antisense oligonucleotides cor more diseases, pulmonary value and for the antisense correctment of diseases and conditions. Typical diseases and conditions correctment of diseases and conditions. Typical diseases and conditions correctment of diseases and conditions. Typical diseases and conditions correctment of diseases, pulmonary vasoconstriction, inflammation, corrective correct asthma, allergies, asthma, impeded respiration, crespiratory distress syndrome, pain, cystic fibrosis, pulmonary corrective corrections of the pulmonary vasoconstriction, emphysema, chronic obstructive correct, hepatocellular carcinoma, kidney cancer, melanoma, hapatic corrects hepatocellular carcinoma, kidney cancer, melanoma, hapatic correct metastasized to the lungs, including breast and prostate cancer.
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Best Local S
Matches 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 114955 BP; 6071 A; 29417 C; 36712 G;
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17-SEP-1997;
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                                                                                                    cgtgtgagctgagcctcgagcacttccaggcgccactggtccgcttcttcctggaggaga
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97US-0059160
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CC The specification describes antisense oligonucleotides (X52869-X55271) CC directed against at least 2 mRNAs selected from target genes, coding and cnon-coding regions at least 2 mRNAs selected from target genes, coding and conding regions are solding regions, intron-exon borders, the coding regions and all segments of RNAs encoding proteins associated with one coding solding and non-coding complete and selected selected with one coding be derived from sequences X55272-74. These multiple target colligonucleotides (specifically X55180-271) can be used for the antisense coding unuleotides (specifically X55180-271) can be used for the antisense coding unuleotides (specifically X55180-271) can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions care those associated with impaired respiration and inflammation, coding lung diseases, pulmonary vasoconstriction, inflammation, coding lung diseases, pulmonary vasoconstriction, inflammation, coding lung diseases, pulmonary vasoconstriction, emphysema, chronic obstructive hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, coding cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as well as all types of cancers which may metastasize or have metastasized to the lungs, including breast and prostate cancer.
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chronic obstructive pulmonary disease; leukemia; lymphoma; car
colon cancer; breast cancer; lung cancer; pancreatic cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 37;
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17-SEP-1997;
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Pred. No. 5.8e-07;
6; Mismatches 990;
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 22-JUN-1998;
17-JUL-1997;
10-OCT-1997;
                                                                                                                                               Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung c
                                               15-JUL-1998;
                                                                      28-JAN-1999
                                                                                                                  Homo sapiens
                                                                                                                                         prostate cancer;
                                                                                                                                                                                    Prostate cancer associated
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98US-0102322.
97US-0896164.
97US-0061599.
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Query Match
Best Local Similarity
Matches 197; Conserv
                                                                                                                       The invention relates to a method for diagnosing a disorder characterise by expression of a human cancer associated antigen precursor coded for be a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifical blinds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and line.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-OCT-1997;
10-OCT-1997;
11-OCT-1997;
                                                                                  Sequence 789
                                                                                                                                                                                                                                                                                                                                                          Claim 67; Page 646; 787pp; English.
                                                                                                                                                                                                                                                                                                                                                                                        New isolated cancer associated nucleic acids and polypeptides isolated using sera from cancer patients, used to develop profor the diagnosis, monitoring or treatment of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen Y, Gout I, Pfreundschuh M,
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     Conservative
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97US-0948705.
97GB-0021697.
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Pred. No. 1.4e
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Scanlan MJ,
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CTGGCTCGTCCCTGCAGGTCCTGCTGGGCTGGGGCCTG
               caggcccccgcccggcaggacctgcaggggacgaaccagccgagagcccatcggagaccc
                                             CTGGCTCGTCCCTGCAGGTCCTGCTGGGCGGGGGCCTGGGGTCTCCGATGGGCTCTCGG
                                                                                         CTGGCTCGTCCCCTGCAGGTCCTGCCGGGGCGGGGCCCTGGGGTCTCCGATGGGCTCTCGG
                                                                                                        CTGGCTCATCCCTTGTAGGTCCTGCCGGGCTGGGGCCTTGGGGTCTCCGATGGGCTCTCGG
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RESULT A10594 ID A1

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Best Local Sim
Matches 160;
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  -tgggagccagggtggccgacaaggtgaggaagcggaggaaggtggtggagggtgctggg
                                                        gnthrthrgthrthrrgvavaasmtgrmtsrashssrassryssrysasnthrcyssras
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Pred. No. 2.2e-
66; Mismatches
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   Nuclear
                     Nuclear Antigen 1 (EBNA 1) DNA.
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plasmid pCMVEBNA;
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Matches 233; Conservative
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P-PSDB; Y28843.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 24; Fig 2;
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06-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0040961
98US-0130114
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/transL_except= (pos:799..800, aa:Gly)
/note= "The sequence is described throughout the
specification as being 1926 nucleotides long, but
sequence of only 1925 bp has been given in figure
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                                                                                                                                                                                                                      Score 71.2; DB 20;
Pred. No. 0.0001;
0; Mismatches 248;
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This sequence is a fragment of the Kaposi's sarcoma-associated herpesvirus (KSHV) LUR (long unique region). This fragment contains coding regions for KI, ORF4 which encodes the complement binding protein v-CBP, ORF6 which encodes a ssDNA binding protein (SSBP), ORF7 which encodes a transport protein, ORF8 which encodes glycoprotein B, ORF9 which encodes OVID-10, ORF10, ORF11, KZ which encodes viral interleukin-6 (vIL-6), ORF02 which encodes dlhydrofolate reductase (DHFR), K3 which encodes BHV4-IE1 I, ORF10 which encodes Thymidylate synthase, K4 which encodes WMIP-I, K7, ORF16 which encodes BHV4-IE1 II, K6 which encodes vMIP-1, K7, ORF16 which encodes BHV4-IE1 II, K6 which encodes vMIP-1, K7, ORF16 which encodes BHV4-IE1 II, K6 which encodes In, ORF18 and ORF19 which encodes Tegument protein I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaposi's sarcoma; acquired immune deficiency syndrome; AIDS; DHFR; Bcl-: dihydrofolate reductase; LUR; long unique region; vaccine; prophylaxis; diagnosis; treatment; HTV8; complement binding protein; v-CBP; SSBP; ssDNA binding protein; transport protein; glycoprotein B; pol; vII-6; DNA polymerase; viral interleukin-6; BHV4-IE1 I; thymidylate synthase; vMIP-II; BHV4-IE1 II; vMIP-I; capsid protein I; tegument protein I; ds.
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di:hydro:folate reductase and is useful for treatment, |
or diagnosis of Kaposi's sarcoma
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                                                                                                                                                                                 KSHV; HHV8; human herpes virus 8; macrophage inflammatory protein
interleukin-6; IL-6; interferon regulatory factor; rheumatoid artl
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                       /product- complement-binding 8699..11236
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13-NOV-1996
the Kapósi's sarcoma-associated herpes virus (KSHY). KSHY is also known as human herpes virus 8 (HHY8). This sequence contains the DNAs of the invention which encode KSHY polypotides selected from: (a) viral macrophage inflammatory protein (MIP) II; (b) viral interleukin-6 (IL-6); (c) viral IRF 1; (d) complement-binding protein; glycoproteins B, M or L; (d) capsid protein IV encoded by ORF65; and (e) immediate early protein
                                                                                                        New nucleic acid encoding Kaposi's sarcoma associated herpes proteins - useful for, e.g. detecting levels of HHV8 in, and preparation of vaccines for treatment of, HIV patients
                                                              This sequence represents the long unique region
                                                                                                                                                                          Bohenzky
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96US-0686343.
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90173..90643
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                                                                                                                                                                                                                                                                                                                                                                                                           1647
                                                                                                                                                                                                                                                                                                                                                                                                                                                      the immune status of a patient infected with HIV. HHV8 derived protein viral MIP III may be used as an anti-inflammatory agent for, e.g. treating rheumatoid arthritis. This sequence is stated as contain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 137507 BP; 32579 A; 37795
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                   ggaggcagcagagttgcaggacgcagaggtgga
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Pred. No. 0.00
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Fusion protein; stabilising polypeptide; proteolytic degradation; resistance; half-life; autoimmune disease; inflammation; nitro drug; IkappaB regulator protein; inflammatory bowel disease; in vivo imaging; nitroreductase protein; enzyme therapy; prodrug therapy; protease;
                                                                                          Nucleotide
                                                                                                                       18-NOV-1998
                                                                                      sequence of the stabilising sequence-encoding
                                                                                                                     (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New fusion proteins resistant to proteolytic degradation comprising a core protein with a stabilising polypeptide
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15-NOV-1996;
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es 229; Conserv
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                   The present sequence is an anti-sense strand of commercially available plasmid pCMYEBNA from which Epstein Barr Virus Nuclear Antigen 1 (EBNA 1) encoding DNA is obtained. EBNA 1 protein is used to stably maintain episomes containing EBV origin of replication (orip) and a gene encoding protein or RNA of interest. Eucaryotic host cells expressing EBNA 1 protein are transfected with these episomes to produce recombinant cell lines expressing multiple genes of interest. This provides a rapid and reliable method of stably expressing multiple genes in transfected cells. The episomes are useful in the transfection of genes encoding receptors, transporter proteins, ion channels adhesion molecules and transcription factors. The episomes carrying desired genes can also be used to transfect cells in gene therapy, antisense therapy, for gene amplification, cell immortalisation, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-sense strand; plasmid pCMVEBNA; EBNA 1; episome; transfection; Epstein Barr Virus Nuclear Antigen 1; origin of replication; EBV oriP; eucaryotic host cell; recombinant cell line; ion channel; multiple gene expression; receptor; transporter protein; gene therapy; transcription factor; adhesion molecule; antisense therapy;
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06-AUG-1998;
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/note= "Epstein Barr Virus Nuclear Antigen
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              of antisense libraries, used for identifying target sites of a selected gene -
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                                                                                  UTAH RES
                                                                 Pierce
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98US-0107504.
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63pp; English
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                                                                                                                                                                                                   identification; multiple cloning
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Pred. No. 0.00057;
0; Mismatches 248;
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                       identifying antisense antisense-mediated
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                                                                                                                                                                                                                                                               gene therapy;
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                                                                                                                                                                                                                                                                                                                                  Vector plasmid
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29; Conservative
                                                                                                                                                Cytomegalovirus. Bos taurus.
                                                                                                                                                                                           Epstein-Barr virus.
Adeno-associated virus.
                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                          e delivery; plasmid pCMVKmITR-EPI;
vaccine; polycationic agent; ss.
/*rag= a
/product= "
2623..4559
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                                                                                                Location/Qualifiers
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Pred. No. 0.00
0; Mismatches
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                          antigen
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nes 248;
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                                                                                                                                                                                                                   This polynucleotide comprises the DNA sequence of vector plasmid CC pCMVKmTTR-EPI, which contains an Epstein-Barr virus (EBV) origin CC of replication from plasmid pCEP4, a coding region for EBV nuclear antigen A from pCEP4, a pair of inverted terminal repeats from CC adeno-associated virus, a cytomegalovirus enhancer/promoter, a CC bovine growth hormone polyA sequence, and a kanamycin resistance selectable marker. Polynucleotides encoding polypeptides, such as CC erythropoietin or leptin, and ribozymes and antisense CC polynucleotides can be inserted into the vector. The vector is preferred for use in novel compositions and methods for improved CC agents are used to increase the frequency of uptake of a nucleic acid (see also V21684-86) into a cell. The polycationic agent can condense with the nucleic acid and inhibit serum and/or nuclease degradation of the nucleic acid and inhibit serum and/or a vector, may express a therapeutic protein or a vaccinating viral CO r cancer antigen, or is itself therapeutic (antisense or ribozyme). The methods and compositions can be used in the gene
                                                                                                                     Query Match 2.9%;
Best Local Similarity 47.7%;
Matches 229; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polycationic agents based on alpha-amino acids, able to complex with nucleic acid - to facilitate its entry into cell, condense it and protect it against serum degradation, particularly for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cohen F, D
Murphy JE,
                               1016
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                                                                                                                                                                                             Sequence 9600 BP; 2326 A; 2376 C; 2817 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 77-80; 100pp; English.
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                                                        Dubois-Stringfellow N, Tetsuo U, Zukermann
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/note= "CMV immediate-early enhancer/promoter"
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/note= "AAV inverted terminal repeat"
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"EBV origin of replication"
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Search completed: October 12, 2000, 18:22:31 Job time: 31809 sec

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 GenCore version Copyright (c) 1993 - 2000
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re greater than or equal to the score of the result being printed,
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1 (Dases 1 to 729)

NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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Plate: LLCM219 row: f column:
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Location/Qualifiers
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/db_xref="taxon:9606"
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96.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: image.llnl. Plate: LLCM97 row: h column: 23 High quality sequence stop: 742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
BE277227
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                                                                                    Similarity
                                                                                                                                                                                       171
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Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM286 row: i column: 17
High quality sequence start: 86
High quality sequence stop: 727.
Location/Qualifiers
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26; Conservative
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/lab_bost="PH108 (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: skin; Vector: pot of pot o
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/db_xref="taxon:9606"
/clone="IMAGE:3618136"
/clone_lib="NIH_MGC_20"
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High quality sequence start: 20
High quality sequence stop: 663.
Location/Qualifiers
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NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                  Similarity
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Tissue_Procurement: ATCC/DCTD/DT
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/ db_xref="taxon:9606"
/ clone=!ib="NIH_MGC_20"
/ clone_!ib="NIH_MGC_20"
/ tissue_type="melanotic melanoma"
/ lab_host="DH108 (phage-resistant)"
/ lab_host="DH108 (phage-resistant)"
/ lab_host="DH108 (phage-resistant)"
/ lone="Organ: skin; Vector: poTB7; Site_1: XhoI; Site_2: ECORI; CDNA made by oligo-dT priming. Directionally cloned into ECORI/XhoI sites using the following 5; adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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RS NIH MGC http://www.ncbi.nlm.nih.gov/MGC/.

RS NIH MGC http://www.ncbi.nlm.nih.gov/MGC/.

RAI Unpublished (1999)

Other_ESTs: 2821312 3prime
Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLML) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LINL at:
www-bio.linl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washingtion Genome Center
Trimming: cross_match from University of Washingtion Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:
http://www.genome.washington.edu
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ha67f02.x1 |
similar to :
element ;, r
AW338856
AW338856.1
EST.
Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                      numan
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33; Conservative
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/lab_host="DHIOB (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRIXTXhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZaP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 210 c 184 g 30 t
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/clone_lib="NIH_MGC_7"
/tissue_type="small cell
/cell_line="MGC3"
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/db_xref="taxon:9606"
                                                                                 606 bp mRNA EST 31-JAN-2000 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2878779 3' TR:096029 096029 7-60. ;contains element MSR1 repetitimRNA sequence.
                                                             GI:6835482
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Chordata;
Primates;
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Pred. No. 1.4e-97;
0; Mismatches 5;
Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                        CAGCCACCAGAAGCCGCGAGGCCCTCAGGGAAGCCCAAGGCCTGCAGAAGCCTCCTGGCC 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: Robert_Strausberg@nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sec
Clone distribution: NCI-CGAP clone distribution in:
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/Image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 421.
Location/Qualifiers
                                                                                                                                                                                                        TCCTCCTGTCCCTGCAGGGGCTGGGGGCTCCGGAGCTGCTGCGGGCTCCCCTCAGGC
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Contact: Robert Strausberg,
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 606)
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref~"taxon:9606"
/clone="IMAGE:2878779"
/clone_lib="NCI_CGAP_Pan1"
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/lab_host="DH10B"
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/db_xref="taxon:9606"
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Pred. No. 3.8e-96;
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                                                                                                     ACTGGCATGCCAAGCCCCTCACGCTCAGGGAGGTCGAGGTGTTTAAAAGCTCCCAGGAGA
                                                                                                                             actggcatgccaagcccctcacgctcagggaggtcgaggtgtttaaaagctcccaggaga
                                                                                                                                                                                                                                                                                                                  TGGAACGAGACTGCAATGGGGACACGCCAAACCTGAGTTTCTACAGAAATGAGATCCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No s1 sequence available.
This clone (DKFZp762B143) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 140
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Canc Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by BMFZ (Biomedical Research Center at the Charite, sequenced by BMFZ (Biomedical Research Center at the Charite, sequenced by BMFZ (Biomedical Research Center at the Charite, sequenced by BMFZ (Biomedical Research Center at the Charite, sequenced by BMFZ (Biomedical Research Center at the Charite, sequenced by BMFZ (Biomedical Research Center at the Charite, sequenced by BMFZ (Biomedical Research Center at the Charite, sequenced by BMFZ (Biomedical Research Center at the Charite, sequenced by BMFZ (Biomedical Research Center at the Charite, sequenced by BMFZ (Biomedical Research Center at the Charite, sequenced by BMFZ (Biomedical Research Center at the Charite).
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1 (Dases 1 to 522)
Koehrer,K., Beyer,A., Mewes,H.W.,
EST (Koehrer, et al.)
Unpublished (1999)
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AL120919.
AL120919.1 GI:5926920 EST.
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/clone_lib="762 (synonym: hmel:
/tissue_type="melanoma (MeWo ca/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSport1; Site_1
a 155 c 148 g 98 t
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/db_xref="taxon:9606"
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Primates;
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Pred. No. 2.5e-94;
0; Mismatches 5;
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similar to
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NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian (Unpublished (1999)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Washington University Genome Sequencing
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40RP from Gibco
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Tissue Procurement: ATCC
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Location/Qualifiers
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/Clone_lib="NIH_MCC_21"
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/lab_host="DH10B (phage-resistant)"
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/note="Organ: placenta; Vector: pOTB7; Sites using the placentionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
08 a 168 c 193 g 57 t
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/db_xref="taxon:9606"
/clone="IMAGE:2963010"
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BE410591.1 GI:
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High quality sequence start: 95
High quality sequence stop: 591.
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Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 591)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian
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Tissue Procurement: ATCC
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Contact: Robert Str
Tel: (301) 496-1550
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3637634"
/clone=libb="NHI_MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="DH1DB (phage-resistant)"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
/site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI,XhoI sites using the
following 5' adaptor: GGCACGG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
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NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)
Other_ESTs: ba97e12.x1
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert-Strausberg@nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Cen
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
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                                                                                                                                                                                                                                                                                BE336852 493 bp mRNA EST 14-JUL-2000 ba97e12.yl NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2957902 5' similar to TR:O96029 096029 7-60. ;, mRNA sequence.
                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 493)
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BE336852.1
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Pred. No. 9.5e-93;
0; Mismatches 3;
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                                        GI:8750809
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//tissue_type="renal cell adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: kidney; Vector: pOTB7; Site_1: XhoI; Site_2: //note="Organ: kidney; Vector: pOTB7; Directionally cloned into EccRI/XhoI sites using the following 5; adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA, synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
03 a 150 c 186 g 53 t 1 others
551 bp mrna
NIH_MGC_20 Homo sapiens cDNA
TR:096029 096029 7-60. ;, mrN
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/clone="IMAGE:2957902"
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Pred. No. 5.3e-87;
0; Mismatches 3;
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gtgacccatgacccacagtgctggcctcctgtggggccactatagcagccaccagaagcc 2229
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                                                                                                         gcgaggccctcagggaagcccaaggcctgcagaagcctcctggcctggctgtgtcttccc 2289
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                                                                                                                                                                        GTGACCCATGACCCACAGTGCTGGCCTCCTGTGGGGCCACTATAGCAGCCACCAGAAGCC 192
                                                                                                                                                                                                                                                              TGCAGGGGCTGGGGCCTCCGGAGCTGCTGCGGGCTCCCCTCAGGCTCTGCTTCGTGACCC
                                                                                     GCGAGGCCCTCAGGGAAGCCCAAGGCCTGCAGAAGCCTCCTGGCCTGGCTTGTCTTCCC 132
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Tissue Procurement: ATCC/DCTp/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 434.
Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 551)
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/db_xref="taxon:9606"
/clone="IMAGE:2905363"
/clone=lib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
CCORI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5;
adaptor: GCCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
96 a 175 c 180 g 100 t
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Pred. NO. 2.8e-86;
0; Mismatches 3;
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Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washingtion Genome Center
Trimming: cross_match from University of Washingtion Genome Center
PHRAP suite: Poly-T identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:
http://www.genome.washington.edu Polyadenylation: Based upon the
presence of a xhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
caaggcgggggaggcagcagagttgcaggacgcagaggtcggagtcttctgccaagtctgg
                                                                 cgagagcccatcggagaccccaggccccagcccggcaggacctacaagggatgagccagc 1997
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Other_ESTs: 2821312.5prime
Contact: Robert Strausberg,
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Plate: LLCM6 row: H column:
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National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                           96
                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DHIOB (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZaP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 173 c 174 g 105 t 2 others
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/clone="IMAGE:2821312"
/clone_1ib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
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Homo sapiens cDNA clone IMAGE:2821312
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                                                                                                                                                                                                                                                                                                                                       Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM293 row: g column: 08
High quality sequence start: 44
High quality sequence stop: 522.
Location/Qualifiers
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1 (bases 1 to 529)

NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

National institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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BE398108
BE398108.1 GI:9343473
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601290328F1 NIH_MGC_8 Homo
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                                                                          /tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph, Vector: poTB7; Site_1: xhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5; adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
04 a 160 c 198 g 67 t
                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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/clone="IMAGE:3620767"
/clone_lib="NIH_MGC_8"
   19.3%;
   Score
Pred.
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 453.6; DB 35;
No. 4.2e-82;
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NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                          Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC
                                                                                                CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can )
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.
plate: LLCM317 row: e column: 21
High quality sequence start: 2
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Mammalia;
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BE409569
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                                                            quality sequence start: 2 quality sequence stop: 532.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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CACTGAACTT
                             ctctgaattt 1274
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/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIXhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
fing Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
a 416 c 389 g 164 t
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Pred. No. 9.8e-80;
0; Mismatches 90
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Local Similarity 92.9%;
nes 577; Conservative
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                                                                               ggcgagccacgagggacatgtgta-ggtatcggcacaactatccgga-tctggtggaacg
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                                                                  GGCGAGCCACGAGGGACATGTGTACGGTATCGGCACAACTATCCGGATTCTGGTGGAACG
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601283311F1 NIH_MGC_44 Homo
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Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian
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mmalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 757)
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3664994"
/clone=lib="NIH_MGC_44"
/clone=lib="NIH_MGC_44"
/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
70 a 204 c 251 g 131 t 1 others
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Pred. No. 2.1e-78;
0; Mismatches 31;
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1: /SIDS1/gcgdata/geneseq/geneseqn/NA1980.DAT:*

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Copyright (c) 1993 - 2000 Compugen Ltd
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22-JUN-1998; 17-JUL-1997; 10-OCT-1997; 10-OCT-1997; 10-OCT-1997; 11-OCT-1997; Chen Y, Gout I, Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer; X40044 standard; DNA; 789 BP 15-JUL-1998; 28-JAN-1999. WO9904265-A2. Homo sapiens. prostate cancer; ss. Prostate cancer associated gene. 02-JUL-1999 (first entry) X40044; (LUDW-) LUDWIG 98US-0102322. 97US-0896164. 97US-0061599. 97US-0061765. 97US-0948705. 97GB-0021697. INST CANCER RES 98WO-US14679 Sahin U, O'Hare M, (Scanlan MJ, Obata Y, C old E;

Pfreundschuh M, Tureci O;

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RESULT 4
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Best Local Similarity

Matches 303; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides encoding human secreted proteins - derived e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries.
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Racie LA,
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Antisense oligonucleotide; multiple target; antisense impaired respiration; inflammation; lung disease;
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Pred. No. 9.7e-47;
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Db 106404 GAGCCAGGGGCCCNNHNNNSCGGGCCGCGGGGCCGAGCCAGGGGCCCNNHNNNSCCGGGC 106345
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CC directed against at least 2 mRNAs selected from target genes, coding and conor-coding regions of RNAs corresponding to target genes, gene cc initiation codons, genomic flanking regions, intron-exon borders, the cc 5'-end, the 3'-end and the juxta-section between coding and non-coding cregions and all segments of RNAs encoding proteins associated with one cc or more diseases, conditions or mixtures. The antisense oligonucleotides considered with one colon proteins associated with one colon proteins associated with one colon conditions. Typical diseases and conditions creatment of diseases and conditions. Typical diseases and conditions care those associated with impaired respiration and inflammation, cc including lung diseases, pulmonary vasoconstriction, inflammation, cc allergic rhinitis, acute asthma, allergies, asthma, impeded respiration, crespiratory distress syndrome, pain, cystic fibrosis, pulmonary consoconstriction, emphysema, chronic obstructive chypertension, pulmonary vasoconstriction, emphysema, chronic obstructive carcinomas e.g. colon cancer, breast cancer, lung cancer, panoreatic carcer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic concer, bepatocellular carcinoma, kidney cancer, melanoma, hepatic cancer, melanoma, hepatic cancer, melanoma, allergies of cancers which may metastasize or have metastasized to the lungs, including breast and prostate cancer.
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Best Local S
Matches 421
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17-SEP-1997;
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Best Local Similarity
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/transl_except= (pos:799..800, aa:Gly)
/transl_except= (pos:799..800, aa:Gly)
/note= "The sequence is described throughout the specification as being 1926 nucleotides long, but sequence of only 1925 bp has been given in figure
                                                                                                                                                                                                                                                                                                                                                                                                                                                      86pp; English
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  The specification describes antisense oligonucleotides directed against at least 2 mRNAs selected from target
                                                                             Disclosure;
                                                                                                                               New antisense oligonucleotides used vasoconstriction
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17-SEP-1997;
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colon cancer; breast cancer; lung cancer; pancreatic cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasoconstriction; emphysema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis;
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coding and

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CC non-coding regions of RNAs corresponding to target genes, gene
CC initiation codons, genomic flanking regions, intron-exon borders, the
CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
CC regions and all segments of RNAs encoding proteins associated with one
CC or more diseases, conditions or mixtures. The antisense oligonucleotides
CC may be derived from sequences X55272-74. These multiple target
CC oligonucleotides (specifically X55180-271) can be used for the antisense
CC are those associated with impaired respiration and inflammation,
CC are those associated with impaired respiration and inflammation,
CC are those associated with impaired respiration and inflammation,
CC allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
CC respiratory distress syndrome, pain, cystic fibrosis, pulmonary
CC hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive
CC carcinomas e.g. colon cancer, breast cancer, lung cancer, panoreatic
CC cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic
CC metastases, as well as all types of cancers which may metastasize or have
CC metastasized to the lungs, including breast and prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.1%; Score 71.2; DB 20; Best Local Similarity 32.0%; Pred. No. 0.00013; Matches 515; Conservative 137; Mismatches 928;
104776 snnndnnccgcbggccbgggcsnnndnnccgcbggccbgggsnnndnnccgcbggccbgg
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RESULT 7
A10594
ID A10594
XX A10594
AC A10594
XX 29-JUN
XX Gene e
XX Gene e
XX Cellul A10594 standard; DNA;

29-JUN-2000 (first entry)

Gene encoding a subunit of cellulose synthase

Cellulose synthase; cellulose production; increase yield; ds

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                                          9458
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(OJIP ) OJI PAPER
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gggaccccgaccacgaggccagcacccagggtcggacctgtgggccagagcatagcaagg
                                      sasnggnhsrargvamtthrargthraasryshsgsrgngashsysgyhssrvaghshss
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RESULT
X40044/c
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DT 02-J
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X40044 standard;

DNA; 789 œ

02-JUL-1999 X40044;

(first entry)

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Query Match
Best Local Similarity
Matches 170; Conser
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17-JUL-1997;
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                            CC Insert. The invention provides a method for increasing the resistance CC inserting onto or into the core protein to proteolytic degradation that comprises linking or CC inserting onto or into the core protein a stabilising polypeptide of CC formula [Glya)X(Glyb)X(Glyc)Z]n where Glya, Glyb, Glyc are 1-6 CC sequential Gly residues and X, Y, Z are Ala, Ser, Val, Ile, Leu, Met, CP Phe, Pro or Thr and n can be anything between 1-66. X, Y and Z need not be identical from n repeat to n repeat. Alternatively a nucleic acid ce nocding the stabilising polypeptide can be linked onto or inserted into CC a nucleic acid encoding a core protein. The fusion proteins of the CC invention are more resistant to degradation by proteases and, thus, have CC used for treating autoimmune diseases, cancer and inflammation. In CC particular, the core protein may be an IxappaB regulator protein for the treatment of inflammatory bowel disease, or a nitroreductase protein which can activate nitro drugs in enzyme/prodrug therapy to treat cancer or other pathological conditions. The fusion proteins can also be used in Very CC diagnostic methods such as in vivo imaging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fusion protein; stabilising polypeptide; proteolytic degradation; resistance; half-life; autoimmune disease; inflammation; nitro drug; IkappaB regulator protein; inflammatory bowel disease; in vivo imaging; nitroreductase protein; enzyme therapy; prodrug therapy; protease; cancer; pathological condition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                              New fusion proteins resistant to proteolytic degradation comprising a core protein with a stabilising polypeptide
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06-AUG-1998;
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/product= "EBNA 1 protein"
/note= "Epstein Barr Virus
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Best Local Similarity
Matches 229; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is an anti-sense strand of commercially available plasmid pCMYEBNA from which Epstein Barr Virus Nuclear Antigen 1 (EBNA 1) encoding DNA is obtained. EBNA 1 protein is used to stably maintain episomes containing EBV origin of replication (orif) and a gene encoding protein or RNA of interest. Eucaryotic host cells expressing EBNA 1 protein are transfected with these episomes to produce recombinant cell lines expressing multiple genes of interest. This provides a rapid and reliable method of stably expressing multiple genes in transfected cells. The episomes are useful in the transfection of genes encoding receptors, transporter proteins, ion channels, adhesion molecules and transcription factors. The episomes carrying desired genes can also be used to transfect cells in gene therapy, antisense therapy, for gene amplification, cell immortalisation, etc.
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ful for gene therapy -
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Antisense; DNA library; inhibition; ss.

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                                                                                                                                                                                                                                                                                                                                                         library targeted to a selected RNA transcript. The methods can be used for identifying antisense agents and for identifying target sites for antisense-mediated inhibition of a selected gene. The use of a direct library for target site selection significantly simplifies the screening process, since only very small libraries need be prepared and assayed. This sequence represents the vector pShuttle which is used in the method of the invention.
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06-NOV-1998;
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                                 ggacccaggaagtgggcggtcaggaccctggggaggcagtgcagccctgccgccaacccc
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                                                                                               This polynucleotide comprises the DNA sequence of vector plasmid pCMVKmITR-EPI, which contains an Epstein-Barr virus (EBV) origin of replication from plasmid pCEP4, a codding region for EBV nuclear antigen A from pCEP4, a pair of inverted terminal repeats from adeno-associated virus, a cytomegalovirus enhancer/promoter, a bovine growth hormone polyA sequence, and a kanamyvin resistance
                                                                                                                                                                                                                                                                                                                             Polycationic agents based on alpha-amino acids, able to complex with nucleic acid - to facilitate its entry into cell, condense and protect it against serum degradation, particularly for use
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Tetsuo U, Zukermann
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selectable marker. Polynucleotides encoding polypeptides, erythropoletin or leptin, and ribozymes and antisense polynucleotides can be inserted into the vector. The vector preferred for use in novel compositions and methods for impolynucleotide delivery into cells. In these methods, polynucleotide delivery into cells.

The vector is

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                                                                                                                                                                                                                                                                               G_i protein coupled receptor; G_iPCR; G_i_a protein; cytoplasmic calcium; calcium mobilization; nociceptin receptor; chemokine receptor; CCR3; CCR2; interleukin 8 receptor type B; episomal expression vector; ss.
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein coupled receptor (G_iPCR) and with a gene coding for a G_i_a protein capable of coupling to the G_iPCR, to increase the cytoplasmic calcium upon binding of an agonist to the G_iPCR. The cell is used to assay a test compound for its effect on a G_iPCR. The method and cells are useful for assaying agonist and antagonist compounds, which bind to G_iPCR which, stimulate intracellular calcium mobilization, such as the nociceptin receptor, and particularly chemokine receptors such as CCR3, CCR2 and the interleukin 8 receptor type B. The present sequence represents the nucleotide sequence of the pCEP4 vector.
                                                                                                                                                                                          6659
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                       Plasmid pCisEBON for subcloning huHGF variants
                                                        31-MAY-1994
                                                                                      Q51731;
                                                                                                                051731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10380 BP; 2560 A; 2561 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A method
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                                                                                                                                                                                                                                                 tggagaagatcgctctgaatttggaggggtgtgccctcagccaggccagcctcaggacgg
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                                                                                                                 standard;
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47.7%;
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Pred. No. 0.00055;
0; Mismatches 248;
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Hepatocyte Growth Factor; HGF;

variant;

mutein;

in vitro mutagenesis;

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Example 1;
                 associated with HGF receptor
                       Hepatocyte growth factor variants cleavage into its two-chain form,
                                              WPI; 1993-386573/48.
                                                                          (GETH ) GENENTECH INC.
                                                                                         18-MAY-1992;
18-MAY-1992;
                                                                                                                17-MAY-1993;
                                                                                                                                            WO9323541-A.
                                                                                                                                                                          misc_RNA
                                                                                                                                                                                                                      promoter
                                                                                                                                                                                                                                                                                              misc_structure
                                                                                                                              25-NOV-1993
                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                         terminator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteolysis resistant; liver; malignancy; CMV-driven;
Cytomegalovirus; episomal expression plasmid; ss.
                                                            Ľď
 Fig 6; 87pp;
                                                            Lokker
                                                                                         92US-0884811.
92US-0885971.
                                                                                                               93WO-US04648
                                                                                                                                                                                                                     /phenotype-
/note- "Tn5
7975..8112
                                                                                                                                                                         8595..10414
                                                                                                                                                                                                                                                                                             /note= "family of repeats" 5866..5978
                                                                                                                                                                                                                                                                        /note- "dyad region"
6375..6457
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4295..4887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= SP6_promoter 845..849
                                                                                                                                                           /label=
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                                                                                                                                                                                                                                                                                                                                                                /function= SV40_origin
1580..4189
                                                                                                                                                                                                                                                                                                                                                                                     /note= "SV40 poly 1108..1531
                                                                                                                                                                                                                                                                                                                                                                                                                                /note- "SP6 RNA start"
902.966
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label= TK_promoter
114..8594
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  English
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                                                            Mark MR
                                                                                                                                                                                                                           neomycin_resistance
neomycin phosphotransferase

    are resistant to proteolytic
used to treat malignancies

                                                                                                                                                                                                                           gene"
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T40348
ID T40348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 229;
                                                                                     Human; hepatocyte growth factor; HGF; huHGF; serum; protection pro-hormone; beta subunit; alpha subunit; kringle domain; plasminogen; catalytic domain; serine protease; HGF variar
                                                                                                                                                                                                    2707
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13-JUL-1993;
18-MAY-1992;
                                                                                                                  Plasmid pCisEBON for expression of hepatocyte growth factor
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                                    20-AUG-1996
                                                                 Synthetic.
                                                                                                                                   09-DEC-1996
                                                                                                                                                 T40348
                                                                                                                                                                T40348 standard;
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                      18-MAY-1992;
                                                   US5547856-A
                                                                               HGF receptor;
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                                                                                                                                  (first entry)
                                                                              malignancy; chronic HGF
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DNA;

10596 BP.

protease; HGF varian receptor activation;

HGF variant;

proteolytic cleavage; prothrombin;

93US-0087783. 92US-0884811. 92US-0884811

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Plasmid pCisEBON (a pRK5 derivative) is an episomal CMV driven expression plasmid. HuHGF variants with enhanced receptor binding activity were produced by site-directed mutagenesis. Stable populations of preferred HGF variants were obtained by transfecting human embryonic kidney 293 cells and then these were subcloned in pCisEBON. See R52940-R52949 for examples of pref. HGF variants.
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ggacccaggaagtgggcggtcaggaccctggggaggcagtgcagccctgccgccaacccc
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920S-0885971 18-MAY-1992;

(GETH) GENENTECH INC

Mark MR Lokker NA, Sodowski PJ,

WPI; 1996-392634/39.

New hepatocyte growth factor variants - are resistant to in vivo proteolytic cleavage into a 2-chain form, useful as HGF antagonists

Example 1; Fig 6; 39pp; English.

This sequence represents the episomal CMV driven expression plasmid pcisEBON which was used in the expression of variant human hepatocyte growth factor HGF). HGF is isolated from human serum and is a disulphide linked heterodimer derived by proteolytic cleavage of the pro-hormone between residues 494 and 495. This generates a molecule composed of an alpha subunit tof 440 annino acids (mol. wt. 69 kD) and beta subunit of 234 amino acids (mol. wt. 34 kD). The alpha and beta subunit sare encoded by a single open reading frame. The alpha subunit contains four kringle domains based on their homology to kringle-like domains in other proteins, e.g. prothrombin, plasminogen. The beta subunit shows high homology to the catalytic domain of serine proteases. However two of the three residues which form the catalytic triad of serine proteases are not conserved in HGF. Therefore, the precise function of the beta chain remains unknown. The invention includes HGF variants which retain HGF receptor binding activity without having the biological activity of wild-type HGF. They can be used for the treatment of pathological conditions associated with the activation of a HGF receptor such as malignancies associated with chronic HGF receptor activation. The pricased for manipulation of the HGF coding sequence and expression of the variant HGF's of the invention.

Sequence 10596 BP; 2627 A; 2571 C; 3023 G; 2375 T; 0 other;

Ĥ 1016 ggacctgtgggccagagcatagcaagggtgg---gggcagggtggacgaggggccccagc 1072 ggggccacggggaagataggccggagcccttaagccccaaagagagcaagaagaagaagc 1192 tggagctgagccggcggagcagccgccacagagccagggcctcagagtgcctcagagg 1252 956 ggaaggtggaggaaggaaggaagccccgggggaccccgaccacgaggccagcacccagggtc 1015 3; Gaps ggacccaggaagtgggcggtcaggaccttggggaggcagtgcagcctgccgccaacccc tgggagccagggtggccgacaaggtgaggaagcggaggaaggtggatgagggtgctgggg tggagaagatcgctctgaatttggaggggtgtgccctcagccagggcagcctcaggacgg Length 10596; Score 67.2; DB 17; Length Pred. No. 0.00055; 0; Mismatches 248; Indels Query Match
Best Local Similarity 47.7%;
Matches 229; Conservative C 1193 1133 2467 1253 1313 Q δ 셤 ŏ 원 δλ 요 ò ద ò 원 ò

Search completed: October 12, 2000, 18:33:26 Job time: 32464 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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/clone="InAGE:3050950"
/clone=Inb="NIH,MGC_20"
/tissue_type="melanotic melanoma"
/tab_host="BAIDB (phage-resistant)"
/note="Corgan: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size=selected >500bp for average insert size 1: 8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (SIratagene) and Superscript II RT (Life Technologies)."
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
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                                       61 ACTGCTGAGGACGCCGATGGCCTGCCTGGCGTGAGGTGACTGTGTGACTGCAGGGTGAC
                                                                            121 TGAGGACGATGGATGTCGGATGCGTGCGTGCGGCGGCTGCGGCCCCAGCTCCTTCCAGT
                                                                                                                                                       ccagaatgacagggtccagaaac-tggcgagccacgaggacatgtgtaggtatcggcac
                                                                                                                                                                                        181 CCAGAATGACAGGGTCCAGAACTTGGCGAGCCACGAGGGACATGTGTAGGTATCGGCAC
                                                                                                                                                                                                                                                                                                        325 agaaatgagatccgcttcctgcccaacggctgtttcattgaggacattcttcagaactgg
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                                                                                                                                                                                                                                                                                                                                                                                   385 acggacaactatgacctccttgaggacaatcactcctacatccagtggctgtttcctctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        481 AAAAGCTCCCAGGAGATCCAGGAGCGGCTTGTCCGGGCCTACGAGCTCATGCTGGGCTTC
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BE387193
BE387193.1 GI:9332558
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104 actgc-gaggacggcgaggcc--
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Local S.
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/db xref="taxon:966"
/clone='IRAGE:3618136"
/clone='IRAGE:3618136"
/clone='IRAGC_20"
/tissue_type="melanotic melanoma"
/lab_host="DB10B (phage=resistant)"
/note="Organ: skin; Vector: polloy: Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size=selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Carladan) using ZAP-cDNA synthesis kit (Siratagene) and Superscript II RT (Life Technologies)."
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                                                                        Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM286 row: column: 17
High quality sequence start: 86
High quality sequence stop: 727.
Location/Qualifiers
1. 751
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 5.1e-110;
0; Mismatches 19; I
                             Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nlh.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.9%;
              Unpublished (1999)
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Matches 626; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
El (bases 1 to 682)
El (bases 1 to 682)
NI Homolitica (1999)
NI Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert-Strausbergenih.gov
Tissue Procurement: ATCC/DOTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCANA88 row: j column: 11
High quality sequence start: 20
High quality sequence stop: 663.
Location/Qualifiers
LCC
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/clone="Lib="NHiMGC_20"
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/tissue_type="melan
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gctcatgctgggcttctacgggatccggctggaggaccgaggcacgggcacggt-gggcc
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Pred. No. 1.1e-108;
0; Mismatches 20;
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BE385629
BE385629.1 GI:9330994
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llarity 96.2%;
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1;
          /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013" a 195 c 204 g 111 t 3 others
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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DKF2p762B143_r1762 (synonym: hmel2) Homo sapiens cDNA clone
DKF2p762B143_5', mRNA sequence.
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   1795 ggacctgcaggggacgagccagccgaggcccatcggagaccccaggccccggcc
                                                                                                                                                                                                                                                            546 -GACCTGCAGGGGACGAGCCAGCNGAGAGCCCATCGNAGACCCANGGCCCCCGCCGGGCA
                                                                                                                                                                                                                                                                                                                                               tcctcctgtccctgctgcaggggctggggcctccggagctgctgcgggctcccctcaggc
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                                                                                                                                                  11; Indels
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Kroehrer, K. Beyer, A., Mewes, H.W., Gassenhuber, J.
EST (Kochrer, et al.)
Unpublished (1999)
Contact: Koehrer K
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
                                                                                                                     21;
                                                                                                                     Score 527.2; DB 2.
Pred. No. 8.2e-97;
                                                                                                                                                0; Mismatches
                                                                 б
/lab_host="DH10B"
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                                                                                                                     23.0%;
ilarity 97.8%;
Conservative
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AUTHORS
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AW338856 GI:6835482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Tel: (301) 465-155
Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
Life Technologies catalog #: 1154@-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAp clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40up from Gibco
High quality sequence stop: 421.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 606)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                          302
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                                                                                                                                                                                          gaactggcatgccaagcccctcacgctcagggaggtcgaggtgtttaaaagctcccagga
           gtccagaaactggcgagccacgagggacatgtgtaggtatcggcacaactatccggatct
                                      GTCCAGAAACTGGCGAGCCACGAGGGACATGTGTAGGTATCGGCACAACTATCCGGATCT
                                                                ggtggaacgagactgcaatggggacacgccaaacctgagtttctacagaaatgagatccg
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/db.xref="taxon:9606"
/clone="IMAGE:2878779"
/clone_lib="NCI_CGAP_Pan1"
/tissue_type="adenocarcinoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     694 tgtgagctgagcctcgagca 713
|| || || || || || 682
663 GTGACCTTGGGCCTCGAGCA 682
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Unpublished (1997)
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TITLE
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/db_xref="taxon:9606"
/dlone="INAGE:2963010"
/clone="INAGE:2963010"
/clone="INAGE:2963010"
/tissue_type="choricoarcinoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: placents, vector: pOTB7; Site_1: XhOI;
/note="Organ: placents, vector: pOTB7; Site_1: XhOI;
/site_2: ECORI; cDNA made by oligo-dT priming.
Directionally cloned into ECORI/XhOI sites using the following 5 adaptor: GCACGGGGG(G). Size-selected >500pp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit
/Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                        CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Washington University Genome Sequencing Conter Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: Image.llnl.gov/Image/Mini/Iresources.shtml
                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 526)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gccgagagcccatcggagaccccaggccccgcccggcaggacctgcaggggacgagcca 1695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1396 gtgaggaagcggaaggaaggtggatgagggtgctggggacagtgctgcggtggccagtggt
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Pred. No. 3.9e-93;
0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. 526
/organism="Homo sapiens"
                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nlh.gov
                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 515.
Location/Qualifiers
                                                                                                                                                                                                                                            Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 22.2%;
Best Local Similarity 98.1%;
Matches 515; Conservative (
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                                                                                       German
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                                                                                                     Genome Project.

No s1 sequence available.

This clone (DKF2p762B143) is available at the R2PD in Berlin.
Please contact the R2PD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.

Location/Qualifiers
             Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by BMFZ (Blomedical Research Center at the Charite, Berlin/Germany) within the cDNA sequencing consortium of the Ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tgaactggcgcagccaccaacaacctccgcatcacacgcatcctcaagtcgccgtgtgagc 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW732857 526 bp mRNA EST 21-APR-2000 bb15910.yl NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963010 5/similar to TR:096029 096029 7-60.;/ mRNA sequence. AW732857 GI:7633196 EST.
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98 t
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Pred. No. 3.8e-94;
0; Mismatches 5; Indels (
                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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/clone="DKF2p762B143"
/clone_lib="762 (synonym: hmel2)"
/tissue_type="melanoma (MeWo cell line)"
/dev_stage="adult"
/lab_lost="DH108"
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155 c 148 g s
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99.0%;
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Matches 517; Conservative
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LOCUS

RESULT AW732857

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421 701 481 ACCESSION VERSION

KEYWORDS

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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergenih.gov
Email: Robert Strausbergenih.gov
Email: Robert Strausbergenih.gov
Ensule Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/Dbrp/Image/Image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 434.
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/db_xref="Laxon:9606"
/dlone='ImAGE:2905363"
/clone='InAGE:2905363"
/clone='Ib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/tab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: poTBT; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACAGG(G). Size-selected >500bp for average
insert size 1:8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
86 a 175 c 180 g 100 t
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Primates; Catarrhini; Hominidae; Homo.
   534
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(Dases 1 to 551)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                        354
                                                                                                                                                                                                      355 tgtttcattgaggacattcttcagaactggacggacaactatgacctccttgaggacaat 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      501 CCCTCACGCTCAGGGAGGTCGAGGTGTTTAAAAGCTCCCAGGAGATCCAGGAGCGCGTT
                                                                                                                                                                                                                                           ccctcacgctcagggaggtcgaggtgtttaaaagctcccaggagatccaggagcggctt
                                                                                           aatggggacacgccaaacctgagtttctacagaaatgagatccgcttcctgcccaacggc
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National Institutes of Health, Mammallan Gene Collection (MGC)

National Institutes of Health, Mammallan Gene Collection (MGC)

National Institutes of Health, Mammallan Gene Collection (MGC)

Contact: Robert Strausberg finh.gov

Tel: (301) 496-1550

Email: Robert_Strausbergfeinh.gov

Tissue Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM337 row: f column: 03

High quality sequence stor: 591.

Plate: LLCM337 row: f column: 03

High quality sequence stor: 591.

Location/Qualifiers

I.: 591.

Actione - Inmems. Homo sapiens."

Actione - Inmems. Homo sapiens."

Actione - Inmems. Homo carcinoma."

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 591)
                                                                                                                                                                                                                                                                                            BE410591 591 bp mRNA EST 21-JUL-2000 601303311F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3637634 5',
55 tccacctgggaggaggacgaggatgcggaggacgcggaggacgaggactgcgaggac 114
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                                                                                     1696 gocgagageccateggagaceccaggeccaggeaggaeet 1740
                                                                                                                       481 GCCGAGAGCCCATCGGAGACCCCAGGCCCCCGCCCGGCAGGACCT 525
                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
BE410591
BE410591.1 GI:9347041
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/note-"Organ: kidney; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGA(G). Size-selected >500Mp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW249563 550 bp mRNA EST 07-JAN-2000 2821312.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821312 3', mRNA sequence.
AW249563.1 GI:6592556
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 (bases 1 to 550)

NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Other_ESTS: 2813112.5prime

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239
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                                                                                                                                                                                                                                                                   ή
                                                                                                                                                                                                                                Length 493;
                                                                                                                                                                                                                              Score 476.2; DB 35; Length
Pred. No. 1.6e-86;
0; Mismatches 4; Indels
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Best Local Similarity 99.0%;
Matches 489; Conservative (
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AUTHORS
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I (Dases 1 to 493)

I (Dases 1 to 493)

INIH-MCC http://www.ncbi.nlm.nih.gov/MGC/.

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INIH-MCC http://www.ncbi.nlm.nih.gov/MGC/.

I (Ontact ESTs: Bas7el2.xl.

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Tel: (301) 496-1550

Email: Robert Strausbergfanh.gov

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin CLIML)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LiNL at:

image.lln!gov/image/html/irssources.shtml

Seq primer: -40RP from Gibco

High quality sequence stop: 423.
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                                                             9agccagccgagagcccatcggagaccccaggccccgccggcaggacctgcaggggac 1869
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                                                                                                  BE336852 493 bp mRNA EST 14-JUL-2000 ba97el2.yl NIH MGC_14 Homo sapiens cDNA clone IMAGE:2957902 5' similar to TR:096029 096029 7-60.;, mRNA sequence. BE336852. GI:9189237
                             Gaps
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                             Indels
         5.9e-87;
                           Mismatches
         No.
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       98.66
                           Conservative
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Matches 479; Conser
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BE336852
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Eukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 529)

NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Tel: (301) 496-1550

Tobal: Robert_Strausbergenih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CONA Library Preparation: Ling Hong/Rubin information can be found through the I.M.A.G.E. Consortium/LiNL at: image.llnl.gov

Plate: LLCN293 row: 9 column: 08

High quality sequence start: 44

High quality sequence start: 44

High quality sequence start: 44

High quality sequence start: 522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: lymph, Vector: porB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/AhoI sites using the following 5' adaptor: GGGAGGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE398108 529 bp mRNA EST 21-JUL-22000 601290328F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620767 5'
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Pred. No. 2.9e-82;
0; Mismatches 3; Indels
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/clone="lib="NH_MGE:3620767"
/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
                                                                                                  BE398108
BE398108.1 GI:9343473
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Best Local Similarity 98.8%;
Matches 490; Conservative (
                                                                                       mRNA sequence.
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/db_xref="taxon:966"
/db_xref="taxon:966"
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/clone='IndeE:821312"
/clone=IndeC_7"
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/cell_line="MoC3"
/lab_host="DH10B (phage-resistant)"
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86 a 173 c 174 g 105 t 2 others
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 1296)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Nopublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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                                              1459 geccagacettggeeettgeegggteeeetgeeceateggggeaeeecaaggetggacae 1518
                                                                                                                                          1519 agtgagaacggggttgaggaggacacagaaggtcgaacgggggcccaaagaaggtacccct 1578
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  0; Mismatches
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/db_xref="taxon:9606"
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High quality sequence stop: 532.
Location/Qualifiers
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  465; Conservative
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Other_ESTS: 2821312.3prime

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert Strausberganih gov
Tissue Procurement: DCTD/DTP CONA Library Preparation: Ling
Tissue Procurement: DCTD/DTP CONA Library Arrayed by: The I.M.A.G.E.

Consortium (LINL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.G.E. Consortium/LML at:

www.bio.lini.gov/Dbrp/image/image than Base Calling / Ouality
Scores: PHRED from University of Washingtion Genome Center. Vertor
Trimming: cross_match from University of Washingtion Genome Center.

PHRAP suite: Poly-T dennification: patwatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:

PHRAP suite: Poly-T dennification: patwatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:

PHRAP suite: Poly-T adentification: patwatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:

PHRAP suite: Poly-T adentification: patwatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:

PHRAP suite: Poly-T adentification: patwatch.pl from Genome Center:

PHAP suite: Poly-T adentification: patwatch.pl from Genome Center:

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High quality sequence stope: 470.

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Action of Macter of General M. Rubin (University of General M. Rubin (University of General M. Rubin (University of Cartagoene) adaptor: GGCAGGGO.

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Callifornia, Berkeley) using Zap-conn synthesis kit

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 546)
                                                                                         ggccagagcatagcaagggtgggggagggtggacgaggggccccagccacggagggtgg 1084
                                          334 GECCAGACATAGCAAGGGTGGGGCA-GGTGGACGAGGGGCCCCAGCCACGGAGCGTGG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 54b)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 4.6e-82;
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96.3%;
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AUTHORS
TITLE
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ORIGIN

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FCORI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 757)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National institutes of Health, Mammallan Gene Collection (MGC)
Unpublished (1999)
                                                                  BE391750 757 bp mRNA EST 21-JUL-2000 601283311F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3504994 5'
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                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert Strausberg@nih.gov
Tissue Procurement: ATCC
                                                                                                                               BE391750.1 GI:9337115
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Matches 577; Conservative
                                                                                                 mRNA sequence.
BE391750
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/tissue_type="choriocarcinoma"
/lab_nost="DH10B (phage-resistant)"
/note="Organ: plase-resistant)"
/inte="Organ: plase-resistant)"
/inte="Organ: plase-resistant)
/inte="Organ: plase-resistant"
/inte_tionally cloned into EcoRI/XhoI sites using the following s' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Strattagene) and Superscript II RT (Life Technologies)."
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669; Conserv
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Human lung tumour Human c-trk oncogene Human PKD1 gene. Human polycystic k Human polycystic k Human polycystic k Human DOBO genomic Human LOBO genomic

Nucleotide sequenc Plasmid pCisEBON f Plasmid pCisEBON f Nucleotide sequenc

Infected cell prot HSV L/ST region. Luciferase gene un

Zinc finger protei The nucleotide seq

Epstein Barr Virus Anti-sense strand Vector pShuttle DN

plasmid pCM

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Human telomerase p FLGA insert stabil

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Result Š. U

Nucleotide sequenc

Rianodin receptor Human LOBO homolog Human gene express Rat Muncl3-1 encod

Human prostate pro cDNA encoding a pr CENP-B cDNA, Homo

Mouse histone H2B

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Cancer associated antigen; diagnosis; research; treatment; human;
breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
prostate cancer; ss.
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V21683
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T94101
T18551
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V05370
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970S-0061765.
970S-0948705.
97GB-0021697.
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Sahin U,
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Pfreundschuh M,
Tureci O;
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10-OCT-1997;
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10-OCT-1997;
11-OCT-1997;
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Prostate cancer as
EST clone BK517.
DNA encoding Pseud
HSV-2 strain SB5 C
                                                                                   Search time 563.62 Seconds (without alignments) 821.150 Million cell updates/sec
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                        Compugen Ltd.
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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                                                                                    October 12, 2000, 18:33:26;
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Listing first 45 summaries
                                                             OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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                                                                                           The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can'be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer; prostate cancer; ss.
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Pred. No. 5.4e-14;
0; Mismatches 11; Indels 3;
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                                                                     Claim 67; Page 646; 787pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prostate cancer associated gene.
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Best Local Similarity 91.5%;
Matches 151; Conservative
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WPI; 1999-132448/11
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10-0CT-1997;
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The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by an unclaid acid molecule (NRM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NRM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; secreted protein; expressed sequence tag; EST; haematopoiesis;
tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic;
receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             499 ggcaggaactgcaggggacgagccagccgagacccatcggagaccccaggccccagccc 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                           isolated using sera from cancer patients, used to develop products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ggaaggacctgcaggggacgagccagccgagaccatcggagaccccaggcccagccc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 789;
                                                                                                                   New isolated cancer associated nucleic acids and polypeptides
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3
                                                                                                                                                            for the diagnosis, monitoring or treatment of cancers
Obata Y, Old
Stockert E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 789 BP; 157 A; 259 C; 275 G; 93 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 103.8; DB 20;
Pred. No. 2.9e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McCoy JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
O'Hare M, O'
Scanlan MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lavallie ER,
Treacy M;
                                                                                                                                                                                                       Claim 67; Page 646; 787pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.4%;
98.1%;
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Gure A,
Sahin U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 105; Conserva
                                                                               WPI; 1999-132448/11.
Chen Y, Gout I,
Pfreundschuh M,
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                                          Tureci O;
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V90541
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polyA_signal
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Matches
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V62176/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   predicted amino acid sequence of ORF2"
                                                                                                                                                                                                                                                                                                                                                                                                                          1064 gggaggcagaagcctgct-gcctggctgtctt-cccacccagctctcccctgcgcccc 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a human expressed sequence tag (EST). The polynucleotide, which is a secreted EST, and the encoded protein are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopolesis regulating activity, tissue growth activity, activin/inhibin activity, chemokinhelic activity, anti-inflammatory activity, caceptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The polynucleotide may also be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                         derived from
                                      New polynucleotides encoding human secreted proteins - derived e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries.
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                                                                                                                                                                                                                                                                                                                                                                   Length 375;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding Pseudorabies virus large latency transcript.
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1..7013
A'rtag a Acrived from PRV strain InFh"
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/*tag* b
/note= "derived from PRV strain Ka"
                                                                                                                                                                                                                                                                                                                     Sequence 375 BP; 56 A; 125 C; 113 G; 81 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                              Query Match 7.7%; Score 94.6; DB 20; Best Local Similarity 91.7%; Pred. No. 1.8e-10; Matches 133; Conservative 0; Mismatches 9;
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/note= "RNA cap site"
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/note= "encodes
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          WPI; 1999-070077/06.
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Q73500
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CILT). The basic sequence is derived from PRV strain InFh and PRV strain Ka. The LIT overlags and is transcribed in the opposite orientation with respect to the EPP (early polypeptide 0) and the immediately early gene (IE180). EPO is nonessential for replicatio. LIT is the only gene expressed during PRV latency, and the IE180 gene is absolutely necessary for PRV replication. However there are 2 copies of IE180 in the genome. It is expected that PRV lacking one 2 copies of IE180 in the genome. It is expected that PRV lacking one 2 copies of IE180 in the genome. It is expected that PRV lacking one 2 copies of IE180 in the genome. It is expected that PRV lacking one 2 copies of these is viable. Deletions in overlapping regions will generate double deletion mutants. The invention is concerned with the construction of attenuated 2 can be achieved by functionally disabiling the expression of the EPO 2 cypen. Can be disrupting the synthesis of the LLT, or both. (See also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5656 ggcggcggcggcggcggggcccgggggcggagggcgagcgagcgggccggggagaggtccga 5715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New pseudorables virus mutants for use in vaccine - having a deletion and/or insertion in the early protein O gene or large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 5.0%; Score 61.8; DB 15; Length 8438; l Similarity 67.4%; Pred. No. 0.00071; 87; Conservative 0; Mismatches 42; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSV-2 strain SB5; immunological response induction; therapy; antiviral identification; viral protein inhibitor; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSV-2 strain SB5 Contig ID 15 DNA sequence.
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V62176 standard; DNA; 117213 BP.
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8382..8387
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### State ### ### ### ### ### ### ### ### ### #	/note- encoded protein shown in W72177 complement (1599616286)	/*tag= r //tag= r //troduct= "ORF#11 protein" //roduct= "encoded protein shown in w72178"	18064)	ت ∍ ت	/*tag= t '/product = "ORF#13 protein" /note= "encoded protein shown in W72180"		/note= "encoded protein shown in W72181" 2015521453 /*tag- v	/product= "ORF#15 protein" /note= "encoded protein shown in W72182" complement (21326.22291)	1		/product= "ONF#17 protein" /note= "encoded protein shown in W72184" 2468425955	/*tag= y /*tag= rose#18 protein w72185" /note= "encoded protein shown in W72185"	complement (2629527251) /*tag= z /broduct= "ORP#19 protein"		7. 5	Comprement (2/0001/04) /*tag= ab //product= "ORF#20a protein"	/note= "encoded protein shown in W/224" complement (3206732735) /*tag= ac	/product="ORF#21 protein" /note= "encoded protein shown in W72187"	3314034984 /*tag= ad //**/10bm#202 profein	/note= "encoded protein shown in W72226" 3338634984	/*tag= ae /product= "ORF#22b protein" /note= "encoded protein shown in W72227"	.37721)	/product= "ORF#23 protein" /note= "encoded protein shown in W72188"	Complement (3803839188) /*tage ag //rcolirt= RPR#24 protein		77
	CDS		CDS	CDS		CDS	CDS	CDS		CDS	CDS		CDS	CDS	340	3	CDS	ļ	CDS	CDS		CDS		cns	CDS	CDS
Location/Qualifiers /*tag a	4 E4 E4	F F F	4 64 64 6	+ E- E- 4 & &	는 등 등 보 14 14	F F F F	ቸዣ ቸዣ	FF FF FF	FT	F F F	ዋዋ ተዋዋ	FT	FE	F F F	4 E E E	. F. F. F.		1 E E	F F F	FT	F F F	FF		1 L L	H H H	

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Kaposi's sarcoma; acquired immune deficiency syndrome; AIDS; DHFR; Bcl-2; dihydrofolate reductase; LUR; long unique region; vaccine; prophylaxis; diagnosis; treatment; HHV8; capsid protein IV; tegument protein IV;
                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a fragment of the genomic sequence containing the coding region for the mouse WRN gene (X83004). The corresponding human gene (X83001) encodes a protein related to Werner's syndrome. The products can be used for the detection and treatment of Werner's syndrome (WS), an autosomal recessive disorder with a complex phenotype,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ggaggaggacgaggatgcggaggacgcggaggacgacgaggactgcgaggacggcgaggc 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acid molecule encoding the WRN gene product -useful for detection and treatment of Werner's syndrome, and related
                                 Mouse; WRN; Werner's syndrome; detection; diagnosis; autosomal; recessive disorder; phenotype; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 58.4; DB 18; Length 51259;
Pred. No. 0.0041;
0; Mismatches 41; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 51259 BP; 14533 A; 9635 C; 10266 G; 16825 T; 0 other;
                                                                                                                                                                                                                                                                   Schellenberg GD,
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             Partial mouse WRN genomic sequence #3.
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                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 7; 153pp; English.
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95US-0009409.
95US-0580539.
96US-0010835.
96US-0594242.
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Best Local Similarity 66.9%;
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             as well as related diseases.
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                                                                                                                                                                                                                                                                                         WPI; 1997-363671/33
                                                                                                                                                                                                                                                                   Fu Y, Mulligan J,
                                                                                                                                                                                                                                (DARW-) DARWIN
(OSHI/) OSHIMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 ggcg 187
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                                                                                                                                                                        29-DEC-1995;
29-DEC-1995;
30-JAN-1996;
                                                                   Mus musculus
                                                                                          WO9724435-A1
                                                                                                                                      30-DEC-1996;
                                                                                                               10-JUL-1997.
                                                                                                                                                             L2-APR-1996;
                                                                                                                                                                                                           30-JAN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                        diseases
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                                 aa: Lys)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "encoded protein shown in W72200"
60759..61151
"encoded protein shown in W72191"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note- "encoded protein shown in W72201"
61241..62071
                                                                                                                                                                                            /note= "encoded protein shown in W72195'
complement (50035..51666)
                                                                                                                                                                                                                                                                                                                                      in W72198
                                                                                                                                                                                                                                                                                                                                                                                   in W72199'
                               /transl_except= (pos: 44063..44064, aa: /product= "Orgets7 protein" /note= "encoded protein shown in W72192 complement (44853..47297)
                                                                                                   in W72193
                                                                                                                                                                                                                                            in W72196
                                                                                                                                                                                                                                                                                         in W72197
                                                                                                                                                 1n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 60; DB 19;
Pred. No. 0.0021;
                                                                                                                                                                                                                                                                 /product="ORF#32 protein"
/note="encoded protein shown
54393..58115
                                                                                      'product= "ORF#28 protein"
'note= "encoded protein shown
                                                                                                                                    /product= "ORF#29 protein"
/note= "encoded protein shown
complement (47305..49662)
                                                                                                                                                                                                                                          /note= "encoded protein shown complement (51701..53575)
                                                                                                                                                                                                                                                                                                                                   /note= "encoded protein shown complement (58060..58977)
                                                                                                                                                                                                                                                                                                                                                                                  /note= "encoded protein shown complement (58970..60760)
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/product= "ORF#33 protein"
                                                                                                                                                                                                                                                                                                                                                            "ORF#30 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                "ORF#36 protein"
                                                                                                                                                                                                                                "ORF#31 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                    'product= "ORF#35 protein'
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                                                                                                              17122..47338
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58.0%;
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/product=
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Matches 105; Conservative
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X83007/c
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WPI; 1998-130615/12
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25-JUL-1996;
25-JUL-1996;
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25-JUL-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KSHV; HHV8; human herpes virus 8; macrophage inflammatory protein II; interleukin-6; IL-6; interferon regulatory factor; rheumatoid arthritis; complement-binding protein; glycoprotein; capsid protein IV; infection;
                                                                                                                                                                                                                                                                               This sequence is a fragment of the Kaposi's sarcoma-associated herpesvirus (KSHV) LUR (long unique region). This fragment contains coding regions for ORF65 which encodes capsid protein IV, ORF66, ORF67 which encodes tegument protein IV, ORF68 which encodes a glycoprotein, ORF69, K12 which encodes immediate early protein (IEP), K14 which encodes cyclin D, ORF73 which encodes immediate early protein (IEP), K14 which encodes ov.2 (v.adh), ORF74 which encodes G-protein coupled receptor, ORF75 which encodes tegument protein/FGART, K15. KSHV is a new human Herpesvirus (HHV8) believed to cause Kaposi's sarcoma (KS) which is the most common form of neoplasm occurring in persons with acquired immune deficiency syndrome (AIDS). The DHFR protein is useful for vaccination, prophylaxis, diagnosis and treatment of a subject with Kaposi's sarcoma and for detecting expression of a DNA virus associated with Kaposi's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 20920 GGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGAGGATGACGAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
glycoprotein; kaposin; cyclin D; immediate early protein; IEP; OX-2; v-adh; G-protein coupled receptor; FGARAT; ds.
                                                                                                                                                                                                                  Kaposi's sarcoma-associated herpes virus nucleic acid - encodes di.hydro:folate reductase and is useful for treatment, prophylaxis or diagnosis of Kaposi's sarcoma
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.6%; Score 56.8; DB 20; Length 32207; 66.1%; Pred. No. 0.008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 32207 BP; 7229 A; 9156 C; 8713 G; 7109 T; 0 other;
                                                                                                                                                                        Russo JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KSHV long unique coding region and terminal repeat.
                                                                                                                                                                       Moore PS,
                                                                                                                                                                                                                                                             Disclosure; Column 155-182; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                 Kaposi's sarcoma-associated herpesvirus.
                                                                                                                                                                       Edelman IS,
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                                                                                                                                                 (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                   96US-0770379.
                                                                                                                          96US-0770379.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 66.1
hes 82; Conservative
                                                                                                                                                                       Chang Y,
                                                                                                                                                                                           WPI; 1999-069741/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                       sarcoma in a cell.
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                                                                                                                                                                       Bohenzky RA,
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                                                                                                   29-NOV-1996;
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                                                                             15-DEC-1998
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Matches
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immediate early protein; Kaposi's sarcoma; protective vaccine; lymphoma; lymphoproliferative disease; leukaemia; splenomegaly; mycosis fungoides; HIV immune status; anti-inflammatory agent; therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                /product- macrophage inflammatory protein II complement (27137..27424)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Russo JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product- interferon regulatory factor 1
28661..29741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product- interferon regulatory factor 4 complement (111931..112443)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product interferon regulatory factor 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'product interferon regulatory factor 3
                                                                                                                                                                                                  'product - complement-binding protein
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/product= immediate early protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= capsid protein IV complement (123808.127296)
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/product= interleukin 6
complement (21548..21832)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= protein T1.1
complement (58976..60175)
                                                                                                                                                                                                                                                                  /product- glycoprotein B complement (17261..17875)
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complement (69412..69915)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= glycoprotein L complement (88410..88910)
                                                                                       Kaposi's sarcoma-associated herpes virus.
                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYCO ) UNIV COLUMBIA NEW YORK
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/*tag= j
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960S-0686349.
960S-0686350.
960S-068814.
960S-0708678.
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/product=
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/product- telomerase protein p105

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This sequence represents the long unique region and terminal repeat of the Kaposi's sarcoma-associated herpes virus (KSHV). KSHV is also known cas human herpes virus 8 (HHV8). This sequence contains the DNAs of the invention which encode KSHV polypeptides selected from: (a) viral complement-binding protein; glycoproteins B, M or L; (d) capsid protein IV encoded by ORF65, and (e) immediate early protein carcoded by ORF73. Labelled probes for the nucleic acid, proteins encoded by it, and antibodies (Ab) specific for the proteins are useful for detecting HHV8. specifically for diagnosis of Kaposi's sarcoma, in body fluids or tissue samples. HHV8 infections can be treated with antisense or triplex forming molecules or agents that bind specifically to the protein. Ab may be used for prophylaxis or treatment of HHV8 infection, while the protein can be used in protective vaccines. Ab may also be used to differentiate between lymphomas, and HHV8 may be implicated in many other lymphoproliferative diseases such as lymphomas, leukaemia, splenomagaly and mycosis fungacides. Cells and animals containing the coules of a patient infected with HHV9. HHV8 derived peptides can be used as targets for antiviral drugs e.g. dihydrofolate reductase gene can be inhibited with methotreake. These can also be used to determine the immune status of a patient infected with HHV9. HHV8 derived protein containing the manner of the immune status of a patient infected with HHV9. HHV8 derived protein containing the election of a patient infected with HHV9. HHV8 derived protein containing the election and a patient infected with HHV9. HHV8 derived protein containing the election of a patient infected with HHV9. HHV8 derived protein containing the election of a patient infected with HHV9. HHV8 derived protein containing the mach as an anti-inflammatory agent for,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 cyccogocgaagagaacgcaggacgcagggaacgaggacgaggagtaggagtcggaggaggagcgagggc 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ggaggaggacgaggaggatgcggaggacgcggaggacgaggactgcgaggacgaggcgaggc 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens mammalian codon-optimized telomerase protein p105 gene.
New nucleic acid encoding Kaposi's sarcoma associated herpes virus proteins – useful for, e.g. detecting levels of HHV8 in, and preparation of vaccines for treatment of, HIV pathents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 137507 BP; 32579 A; 37795 C; 35758 G; 31375 T; 0 other;
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ed. No. 0.0093;
Mismatches 40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 telomerase; p105; treatment; prevention; cancer; restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 56.8;
Pred. No. 0.
                                                                                                  Example 2; Page 135-203; 230pp; English.
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Matches 82;
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V13836
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The sequence is that of a human telomerase protein coding sequence codon-optimized for mammalian cell expression. The sequence, or specific fragments of it, can be used to modulate expression of a telomerase transcript (by hybridising to it intracellularly), e.g. telomerase transcript (by hybridising to it intracellularly), e.g. for treatment or prevention of cancer, restenosis, inflammation, myocardial infarction, glomerulonephritis, transplant rejection and infections (e.g. with human immunodeficiency virus). It can be used to express recombinant telomerase protein which can be used to screen for agents, e.g. antibodies, that modulate binding of human telomerase cotis binding target. Those that inhibit telomerase activity can be used to treat the conditions listed above, while those that are used to treat the conditions listed above, while those that are used to treat the conditions listed above, while those that are compliant proteins lower at some season of hypersensitivity or atrophy, also to improve production of recombinant proteins by maximising cells density and survival and expansion of precursor cells being used for bone marrow transplants.

They may also be used for diagnosis. other uses of telomerase proteins are isolation, enrichment and concentration of telomerase RNA or proteins; as immunogens; in therapy; as reagent where nascent oligonachecities of known structure are needed (e.g. for tagging native nucleic acid molecules) and for regulating cell growth/density colerance. The agents and the telomerase proteins should be very expectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               657 gaagaagggccgcgaggaggaggacatggaggaggaggagaacgacgacgacgacgacga
                                                                                                                                                                                                                                                                                                                                      nucleic acid encoding human telomerase protein p105 or its ments - used for therapeutic modulation of telomerase activity for screening for potential modulators of telomerase-target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ggaggaggacgaggatgcggaggacgcggaggacgaggacgaggactgcgaggacggcgaggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 717 cgacgacgaggaggacggcgtgttcgacgacgaggacgaggaggaggagaacatcgagag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cggcgcggcccagctccagtccagaatgacagggtccagaaactgg--cgagccac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 caaggtgaccaagcccgtgcagatccagaagcgcgccgtgaagcgccccgcccaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gagggacatgtgtaggtatcggcacaactatccggatctggtggaacgagactgcaatgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2277 BP; 557 A; 723 C; 781 G; 216 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 56; DB 19;
Pred. No. 0.0086;
0; Mismatches 120,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ggacacgccaaacctgagtttctacagaaatgag 334
                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Pages 24-25; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.5%;
illarity 55.1%;
Conservative
                                                                                                                   97WO-US12297
                                                                                                                                                         960S-0676967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                 (TULA-) TULARIK INC
                                                                                                                                                                                                                                                                                 WPI; 1998-101044/09
                                                                                                                                                                                                                                                                                                                                        Tragments - used
                                                                                                                                                                                                                                                                                                    P-PSDB; W41927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            somatic cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Simil
Matches 151; (
                                     WO9801543-A1
                                                                                                                   08-JUL-1997;
                                                                                                                                                         08-JUL-1996;
                                                                             15-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                       binding
                                                                                                                                                                                                                                         Cao Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               777
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Cocation/Qualifiers

Homo sapiens.

Synthetic

Key

/*tag=

240

300 896

837

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ogaggagctggcccagagcgacaccagcagg 930 301 ggacacgccaaacctgagtttctacagaaatgag 334

897

BP

X83006/c ID X83006 standard; DNA; 16442

776

cgacgacgaggaggacggcgtgttcgacgaggaggacgaggaggaggagaacatcgagag cggcgcgcccagctccagtccagaatgacagggtccagaaactgg--cgagccac caaggtgaccaagcccgtgcagatccagaagcgcgccgtgaagcgccccgcccaa 241 gagggacatgtgtaggtatcggcacactatccggatctggtggaacgagactgcaatgg

717 183 111

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gaagaagggccgcgaggaggaggacatggaggaggaggagaacgacgacgacga

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This polynucleotide comprises a synthetic RNA sequence coding for the p105 subunit (see W45593) of human telomerase and optimised for expression in mammalian cells. It is based on an isolated conx expression in mammalian cells. It is based on an isolated conx colone (see V05369) for p105. The invention provides methods relating to human telomerase and related nucleic acids, including the subunit proteins p140, p105, p48 and p43. The proteins may be produced recombinantly from transformed host cells or purified from human cells. Also included are human telomerase RNA (see V05373) and functional derivatives (see V05374 and V16092-93), as well as p105 synthetic DNA sequences (V05370-72). The invention also provides isolated telomerase hybridisation probes and primers capable of specifically hybridising with the telomerase gene, telomerase specific binding agents such as specific antibodies, and methods of making and using the subject compositions in diagnosis (e.g. gene therapy to modulate telomerase transcripts), therapy (e.g. gene therapy to modulate telomerase transcripts), therapy chemical libraries for lead agents). Modulation of telomerase expression can be used for the treatment or prevention of cancer, expression can be used for the treatment or prevention of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding human telomerase proteins or their fragments - useful for therapeutic modulation of telomerase activity and for screening for potential modulators of telomerase-target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myocardial infarction, glomerulonephritis
                                                                                                                                                                                                                                                               Telomerase; p105; human; cell replication; cancer; restenosis; multiple sclerosis; inflammation; rheumatoid arthritis; myocardial infarction; glomerulonephritis; transplant rejection; infection; therapy; ds.
                                                                                                                                                                                                                             Human telomerase p105 subunit mammalian optimised synthetic RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2277 BP; 557 A; 723 C; 781 G; 216 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infections (e.g. with HIV)
Disclosure; Page 23-24; 32pp; English.
                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0676974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-US12296
                                                                                                           V05372 standard; RNA; 2277
                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transplant rejection or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-101043/09
                                                                                                                                                                                                                                                                                                                                                               sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                  WO9801542-A1
                                                                                                                                                                                     06-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collins K;
                                                                                                                                                 V05372;
                                                                       10
                                                                       RESULT
                                                                                           705372
                                                                                                                               g
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detection; diagnosis; autosomal; ss.

Partial mouse WRN genomic sequence #2.

(first entry)

31-AUG-1999

x83006;

Mouse, WRN; Werner's syndrome; recessive disorder; phenotype;

WO9724435-A1

Mus

10-JUL-1997

Mouse; WRN; Werner's

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the coding region for the mouse WRN gene (x83004). The corresponding human gene (x83001) encodes a protein related to Werner's syndrome. The products can be used for the detection and treatment of Werner's syndrome (WS), an autosomal recessive disorder with a complex phenotype,
                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a fragment of the genomic sequence containing
                                                                                                                                                                                                                                                                                                                                              related
                                                                                                                                                                                                                                                                                                                                Isolated nucleic acid molecule encoding the WRN gene product useful for detection and treatment of Werner's syndrome, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16442 BP; 4392 A; 2975 C; 3408 G; 5665 T; 2 other;
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                                                                                                                                                                                                                                                                                         Schellenberg GD,
                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 7; 153pp; English.
                                                                                                                                                                                                                                                                                         Oshima J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                as well as related diseases.
                                                                                                                                                                                                                                                                                                           WPI; 1997-363671/33.
                                                                                                                                                                                                                                                                                       Fu Y, Mulligan J,
                                                                                                                                                                                                                                                                     OSHIMA
                                                                                                                                                                                                                                                                                                                                                      diseases
                                                                                                                                                                                                                                                                    (OSHI/)
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MOLECULAR CORP

DARWIN

(DARW-)

96US-0594242

96US-0632175. 95US-0009409. 95US-0580539. 96US-0010835.

96WO-US20785

30-DEC-1996;

12-APR-1996, 29-DEC-1995, 29-DEC-1995 30-JAN-1996 30-JAN-1996 ö

Gaps

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4.5%; Score 56; DB 18; Length 16442; 64.8%; Pred. No. 0.011; .ive 0; Mismatches 45; Indels 0;

Conservative

Query Match Best Local Similarity Matches 83; Conserv

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Gaps

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ggaggaggacgaggatgcggaggacgcggaggacgaggactgcgaggacggcgaggc 123

4.5%; Score 56; DB 19; Length 2277; 55.1%; Pred. No. 0.0086; ive 0; Mismatches 120; Indels :

Conservative

Similarity

Local Simmes 151;

Best Loca Matches 64

δλ

Query Match

363 gacgacgccatggttgcgatggtcag 388

170 gaggagccgcgggcggcgccag

셤 ò 셤 Systematic peptide evolution by reverse translation; SPERT; ligand; specific; inhibitors; probes; assay; cell sorting; ss.

PCR primer for 5' fixed sequence contg. T7 promoter and RBS

(first entry)

22-JUN-1993

036859;

Q36859 standard; DNA; 390

RESULT 13

036859 ID 03

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The sequence is that of an example randomising oligonucleotide which is used in the prepn. of mRNA encoding candidate polypeptides for the method of systematic polypeptide evolution by reverse translation (SPERT). The method provides a rapid way of isolating and identifying polypeptide ligands which bind to target mols. The polypeptide ligands can be used in e.g. assay methods, diagnostic procedures, cell sorting, as activators or inhibitors of target mol. function, as probes, as sequestering agents, drug delivery vehicles, modififers of hormone
                          ggaggaggacgaggatgcggaggacgcggaggacgaggactgcgaggacggcgaggc 123
                                                        Systematic polypeptide evolution by reverse translation; SPERT; ligand binding; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New method of systematic polypeptide evolution by reverse translation - by linking each polypeptide in sample mixt. tindividualised mRNA allowing further synthesis of selected
                                                                                                                                                                                                                                                                                                     Randomising oligonucleotide used in SPERT mRNA prepn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 390 BP; 125 A; 126 C; 133 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              action and as catalysts. See also Q21830-Q21832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example; Page 55; 102pp; English.
                                                                                                                                                                                                                Q21833 standard; DNA; 390 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                91WO-US05463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90US-0561968
                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (COLS ) UNIV OF COLORADO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-080018/10.
                                                                                                                                           16241 GGAGGAGC 16234
                                                                                                              184 ggcgcggc 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tuerk C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide(s)
                                                                                                                                                                                                                                                                       08-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                     WO9202536-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   20-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sold L,
                                                                                                                                                                                                                                            021833;
                                                                                                                                                                                     RESULT 12
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64
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Systematic polypeptide evolution by reverse translation - used for prodn. of polypeptide ligand specific for desired target

Example 1; Page 84; 98pp; English.

molecule

ပဲ Tuerk

Smith JD,

Gold L,

WPI; 1993-076529/09

(UYRE-) UNIV RES CORP. Pribnow D,

92WO-US00801. 91US-0739055

31-JAN-1992; 01-AUG-1991;

WO9303172-A. 18-FEB-1993,

Synthetic.

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of the epitope commonly recognised by the antisers from autoimmune mice which are the fl progeny of a cross of N2B and N3W parents (Portanova et al., J. Immunol. 144, 4633, 1990). The known epitope consists of ca. 10 aniho acids at the N-terminus of the histone H2B protein. To make mRNA encoding candidate polypeptides a 5' fixed sequence composed of a 77 promoter sequence and a ribosome binding site which is recognised by both prokaryotic and eukaryotic ribosomes, terminating in a restriction endonuclease site is synthesised and cloned using a number of oligonucleotides (example shown). A 3' fixed sequence is placed into a restriction site to provide an mRNA encoding the C terminal trailer sequence of ca. 100 nucleotides lacking stop codons. In addition, a' primer annealing site is provided so that CDNA synthesis can be accomplished on the mRNA recovered from partitioned ribosome complexes. See also Q36845-63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 gncgactccacctgggaggaggacgaggaggatgcggaggacgcggaggacgaggactgc 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPERT is used to select novel polypeptides that bind the antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 390 BP; 125 A; 126 C; 133 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 55.4; DB 14;
Pred. No. 0.0093;
0; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 61.0
nes 89; Conservative
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Gaps

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Indels

57; DB 13;

Score 55.4; DB 1 Pred. No. 0.0093; 0; Mismatches 5

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4.5%; ilarity 61.0%; Conservative 0

Best Local Similarity Matches 89; Conserv

20

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110

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a

Query Match

Length 390;

gnegactecacetgggaggaggaegaggaggatgeggaggaegeggaggaegaggaetge 109

BP

gg 123

(first entry)

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N-terminal; prostate tumour cell; immunogenic; treatment; diagnosis; prostate cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated prostate polypeptides useful for the treatment, diagnosis and monitoring of prostate cancer
                                                                                                                                                                                                   cDNA encoding a prostate tumour cell polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 28; Page 78-79; 106pp; English.
                                                                                                                           X35871 standard; cDNA; 768
                                                                                                                                                                                                                                                                                                                                                                                                                     Dillon DC, Mitcham JL,
                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-277272/23.
                                                                                                                                                                                                                                                                                    WO9918210-A2
                                                                                                                                                                          13-JUL-1999
                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                   J7-0CT-1998;
                                                                                                                                                                                                                                                                                                                                                           23-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                       07-OCT-1997;
                                       189 99 190
                                                                                                                                                                                                                                                                                                            15-APR-1999.
                                                                                                                                                  X35871;
                                                                                                   RESULT 15
X35871
                                                                 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This cDNA sequence includes a coding region for human prostate protein HPA8 (see W23322), an immunogenic portion of which can be used in a claimed pharmaceutical composition for the treatment of prostate cancer, in a claimed vaccine for treatment of prostate cancer, or to raise claimed antibodies suitable for use in claimed state and antibodies suitable for use in diagnosis or monitoring the progression of prostate cancer. HPA8 cDNA was isolated from a human prostate adenocarchnoma cell line LnCap.igc (ATCC CRL-1740) cell cDNA library by expression screening with human prostatitis sera. DNA sequences (see T84927-52) for I7 HPA proteins (see W2313-23 and W27303-07) are provided and can be used to produce recombinant HPA polypeptides in host cells

( Particularly E. coli, yeast and mammalian cell lines) and to design primers and probes for use in claimed methods of detecting
                                                                                                                                                                                 cancer; immunotherapy; therapy; immunodiagnosis; diagnosis; human; HPAB; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunogenic portions of prostate proteins - useful to develop products to detect, monitor, treat or inhibit development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 768 BP; 198 A; 164 C; 220 G; 185 T; 1 other;
                   363 gacgaccatggttgcgatggtcag 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 28; Page 64-65; 84pp; English.
170 gaggagccgcgggcggcggcccag 195
                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                              Twardzik DR;
                                                                                                                                                        Human prostate protein HPA8 cDNA
                                                                                 T84941 standard; cDNA; 768 BP
                                                                                                                                                                                                                                                                                                                                                                 96US-0633840.
96US-0616745.
                                                                                                                                                                                                                                                                                                                                           97WO-US04192
                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                              Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-470816/43.
P-PSDB; W23322.
                                                                                                                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   products to dete
prostate cancer
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                                                                                                                                  27-APR-1998
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                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                           14-MAR-1997;
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15-MAR-1996;
                                                                                                                                                                                                                                                                                                                   18-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                           Dillon DC,
                                                                                                                                                                                 Prostate
                                                                                                                                                                                            vaccine;
                                                                                                         T84941;
                                                          RESULT 14
                                                                       r84941
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Twardzik DR;

Reed SG,

98WO-US21166. 98US-0102679. 97US-0946026.

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The present sequence encodes a polypeptide obtained from prostate tumour cells. The polypeptide comprises an immunogenic portion of a prostate protein. The polypeptides and DNA obtained from prostate tumour cells, as well as antibodies raised against the protein, can be used in the treatment, diagnosis and monitoring of prostate
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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/ Organism="Homo sapiens"

/ Ab_rate="Laxan:9606"

/ Clone=lib="NIH_MGC_20"

/ Clone=lib="NIH_MGC_20"

/ Clone=lib="NIH_MGC_20"

/ Lab_host="DH10B (phage-resistant)"

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at: image.llnl.gov
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High quality sequence stop: 742.
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                                                                                                                                                                                128 GATGGATGTCGGATGCATGCCTGCGTGGCGCTGCGGCCCAGCTCGTTCCAGTCCAGAAT
                                                                                                                                                                                                                                     GACAGGGTCCAGAAACTTGGCGAGCCACGAGGGACATGTGTAGGTATCGGCACAACTATC
                                                                                                                                                                                                                                                                                                                                                                    actatgacctccttgaggacaatcactcctacatccagtggctgtttcctctgcgagaac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          728 GAGACGCTGGTGCGGGGTGAGCTGCCGGGGGGTGCCGGCAGAGGTGCCTGGGACTTAC
                            30;
  Length 868;
                            74; Indels
  DB 34;
 Score 577.6; DB 34
Pred. No. 9.8e-119;
0; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE387193 751 bp mRNA 601277069F1 NIH_MGC_20 Homo sal mRNA sequence.
BE387193
BE387193.1 GI:9332558
EST.
46.98;
              Best Local Similarity 87.9
Matches 752; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cacttccggccccgct
||| ||| ||| ||| |
GCCTTTCGGGCCCGGT
                                                                                                   111 aggacggcgaggcc-
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VERSION
KEYWORDS
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4

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/issue__iype="choicarcinoma"
/lab_host="DulOB (phage=resistant)"
/note="Organ: placenta; Vector: poTB7; Site_1: XhoI;
/note="Organ: placenta; Vector: poTB7; Site_1: XhoI;
Site_2: EcoRI; CoNBA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGAGGG(G). Size=selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (base 1 to 591)

NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Pari: (301) 496-11550

Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                           BE410591 591 bp mRNA EST 21-JUL-2000 601303311F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3637634 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   con Library Preparation: Ling Hong/Rubin Laboratory con Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: Image.llnl.gov Plate: LLCM337 row: f column: 03 High quality sequence start: 95 High quality sequence stop: 591.

Location/Qualifiers
                                                                                                                                   648
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llarity 99.4%; Pred. No. 7.5e-103;
Conservative 0; Mismatches 3; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .591
/organism="Homo saplens"
/db_xref="taxon:9606"
/clone="IRAGE:3637634"
/clone=lib="NIH_MGC_21"
                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
BE410591
BE410591.1 GI:9347041
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
JOURNAL
COMMENT
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                 499
                                                       531
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                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 751)

National Institutes of Health, Mammalian Gene Collection (MGC)

Oupublished (1999)

Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov

Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov

Tissue Preparation: Ling Hong/Rubin Laboratory

CONA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Information can be found through the I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Libra at: image.llnl.gov

Plate: LLCM286 row: 1 column: 17

High quality sequence stop: 77.

Location(Vaulifiers

1. 751

/doranism="Homo sapiens"

/db.xref="taxon: $606"

/clone_libra: MAGE: 3618136"

/clone_libra: Mah. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of california, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Tephnologies)."

NAT 170 a 202 c 254 g 125 t
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Pred. No. 4.8e-117;
0; Mismatches 0;
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Best Local Similarity 99.5
Matches 603; Conservative
                 Homo sapiens
               ORGANISM
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ORIGIN
                                                                     REFERENCE
AUTHORS
TITLE
JOURNAL
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VERSION
KEYWORDS
                                                                                                                                                                                    342
                                                                                                                                                                                                                                                                                                                                          522
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TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz- heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 522)

Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.

Est (Koehrer, et al.)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No s1 sequence available.
This clone (DKFZp762B143) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcentrum, Heubnerweg 6, 14059
Berlin-Charlottenbug, GFEMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                      415
                                                                                                                                                                                                            cccttcacgcttcagggaggttcgaggtgtttaaaagctcccaggagatccaggagcggtt 535
                                                                                                                                                                                                                                                                                                                                                                                                                        AL120919 522 bp mRNA EST 25-FEB-2000 DKF22P/62B143_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKF20762B143 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : pSport1; Site_1: Not1; Site_2: Sall"
148 g 98 t
cactectacatecagtggetgttteetetgegagaaceaggagtgaactggeatgceag
                                                                                                                                                                                                                                                            gccacgagggacatgtgtaggtatcggcacaactatccggatctggtggaacgagactgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .522 /organism="Homo sapiens" /db_cref="taxon:9606" /clone="DKEZP762B143" /clone=lib="762 (synonym: hmel2)" /dev. stage="adult" /dev. stage="adult" /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                   /note-"Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL120919.1 GI:5926920
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AUTHORS
TITLE
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COMMENT
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SM Homo sapiens
Eukaryota, Mammalia; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
La (Dases 1 to 729)
RS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
AL Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Fmail: Robert_Strausberg@nih.gov
Plate: LLCM219 row: f column: 18
High quality sequence stop: 627.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                               BE264806 729 bp mRNA EST 13-JUL-2000 601192867F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3536657 5',
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   Length 522
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/db_xref="taxon:9606"
/clone="IMAGE:3536657"
/clone=lib="NHLMGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 502; DB 14;
Pred. No. 6.4e-102;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
BE264806
BE264806.1 GI:9138366
 40.7%;
98.9%;
                               Conservative
                Similarity
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cctgaactgg 648
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                                                                                                                                                                                                                                                                                                                                                                                                                       al Similarity
570; Conserv
                                                                                                                                                                                                                                                                                                                                       170
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Best Local S:
Matches 570)
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                                                                                      FEATURES
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                                                                                                                                                                                                                                      1;
/note="Organ: lung; Vector: poTB7; Site_1: Xho1; Site_2: ECORI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/Xho1 sites using the following 5' adaptor: GGCAGGAGGG. Size-selected >500bpf for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SM Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaliai; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 757)
S NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergenih.gov
Tissue Procurement: ATC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ú
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       525 aggagoggettgteegggeetacgageteatgetgggettetacgggateeggetggagg 584
                                                                                                                                                                                                                                                                                                                                     accgaggcacgggcacggtgggccgaggcacagaactaccagaagcgctt-cagaacctga 643
                                                                                                                                                                                                                                                                                                                                                        actggcgcagccacaacaacctccgcatcacacgcatcctcaagtcgccgtgtgagctga 703
                                                                                                                                                                                                                                                                                                                                                                                                                                      121 ACTGGCGCAGCCACAACAACCTCCGCATCACGCATCCTCAAGTCGCTGGGTGAGCTAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tcgtctgggggccccaagacaagctgcggaggttcaagcccagctctctgccgcatccgc 943
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                      BE391750 757 bp mRNA EST 21-JUL-2000
601283311F1 NIH_MGC_44 Homo sapiens CDNA clone IMAGE:3604994 !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gacaccagogocogocagotggtgcacttcgcctgggagcacttccggccccgctgcaagt
                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                  Score 437.6; DB 34; Length 729;
Pred. No. 1.4e-87;
0; Mismatches 9; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       944 tcgagggctccaggaaggtggaggaggaaggacctgcaggggac 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCGAGGGCTCCAGGAAGGTGGAGGAGGAAGGAAGCCCCGGGGAC 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
BE391750
BE391750.1 GI:9337115
                                                                                                                                                                                                     35.5%;
97.8%;
                                                                                                                                                                                                                     Best Local Similarity 97.8
Matches 454; Conservative
                                                                                                                                     151
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                                                                                                                                                                                                       Query Match
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BE391750
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                   BASE COUNT
                                                                                                                                                                                                                                                                                                                                       585
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AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                      61
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/organism="Homo sapiens"
/db_xref="Laxon:9606"
/dlone="lib="NIH_axon:9606"
/clone="lib="NIH_axon:9606"
/clone="lib="NIH_axon:9604"
/tlssue_type="endometrium, adenocarcinoma cell line"
/tlab_host="bhl08 (phage=resistant)"
/lab_host="bhl08 (phage=resistant)"
/note="Organ: uterus; Vector: pOrg8; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 's
adaptor: GGCAKCGAG(G). Library constructed by Ling
in the laboratory of Gerald M. Rubin (University of
california, Berkeley) using ZaP-cDNA synthesis Rit
(Stratagene) and Superscript II RT (Life Technologies)."
// O a 204 c 251 g 131 t l others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 ggagccgcgggcgg-cgcggcccagctccagtccagaatgacagggtccagaaact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ccaggagcggcttgtccgggcctacgagctcat-gctgggcttctacgggatcc-ggctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCAGGAGCGCCTTGTCCGGGCCTACGAGCTCATAGCTGGGCTTCTACGGGATCCGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ggcatgccaaagcccc.tcacgctcaggga-ggtcgaggtgtttaaaagctcccaggagat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 757;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 430.8; DB 35; Length
Pred. No. 4.7e-86;
0; Mismatches 27; Indels
found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
Plate: LLCM25z row: f column: 03
Plate: LLCM25z row: f column: 03
High quality sequence start: 110
High quality sequence stop: 686.
                                                                                             Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.08;
93.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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and 3' adaptor sequence:
5'-GAGAGAGACTCGAGTTTTTTTTTTTTTTTT3'. The library was size-selected for >0.5 kb inserts and has an average insert size estimated at 1.2 kb. This library was constructed using the CAP-trapper method for full-length was constructed by Dr. Claudio Schneider (LNCIB-Area Science Park, Trieste, Italy).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 432)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: brain; Vector: pBluescript SK (Stratagene); Site_1: Sstt. Site_2: Xho!; Double-stranded cDNA was prepared from human fetal brain tissue. 5' and 3' adaptors were used in cloning as follows: 5' adaptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@inage.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 431.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALBIG189 432 bp mRNA EST 09-JUL-1999 au45h07.x1 Schnelder fetal brain 00004 Homo sapiens cDNA clone IMAGE:2517757 3', mRNA sequence.
                                                                                                                                        184 CCAGAATGACAGGGTCCAGAAACTGGCGAGCCACGAGGGACATGTGTAGGTATCGGCACA 243
                                                                                       244 ACTATCCGGATCTGGTGGAACGAGGTGCAATGGGGACACGCCAAACCTGAGTTTCTACA 303
                                            actatocogatotogtogaacgagactgcaatgoggacacgccaaacctgagtttctaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Schneider fetal brain 00004"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="frontal lobe"
/dev_stage="5 months post-conception"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2517757"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
Other_ESTs: au45h07.y1
Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                   447 gagaaccagg 456
                                                                                                                                                                                                                                                                                                                                                                                  424 GAGAACCAGG 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human.
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AI816189/c
LOCUS
DEFINITION
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ORGANISM
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                                               267
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KEYWORDS
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Hopkins University)."

3 18 c 151 g 63 t
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                                                                                                                                                                                                                                                                                                     1 (bases 1 to 433)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Gelsel, G., Jost, S.,
Kirzman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin
'J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
Wash To human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
Mashington University School of School of Medicine
Tel: 314 286 1800
Fex: 314 286 1810
                                            A1459806 433 bp mRNA EST 09-MAR-1999 apl7911.x1 Schiller oligodendroglioma Homo sapiens cDNA clone IMAGE:1955684 3' similar to contains element MSR1 MSR1 repetitive
                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         caggggacgaggacgaggagtcggaggagccgcgggcgcggcccagctccagt 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ccagaatgacagggtccagaaactggcgagccacgagggacatgtgtaggtatcggcaca 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 CAGGGGACGAGGACGAGGAGTCGGAGGAGCCGCGGGCGGCGCGGGCCCAGCTCCATTCCAGT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 gocgagoatggacgaccocgactgnogactccacctgggaggaggacgaggatgcgg 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 eccenecargeaceacccceeerg-ceacrccaccreegaggaggaggaggaggargceg 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10; Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 414.8; DB 10; Length
Pred. No. 1.7e-82;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ixAGE:1955684"
/clone=lib="Schiller oligodendroglioma"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="oligodendroglioma"
/dev_stage="44 years"
/lab_host="SOLR"
                                                                                                          element;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.7%;
99.3%;
                                                                                                                                                               AI459806.1 GI:4312687
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Matches 427; Conservative
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                                                                                                                                        ACCESSION
VERSION
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JOURNAL
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RESULT
AI459806
                                                                                                                                                                                     KEYWORDS
SOURCE
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 549)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               506 aaaagctcccaggagatccaggagcggcttgtccgggcctacgagctcatgctgggcttc 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE391975 549 bp mRNA EST 21-JUL-2000
601285002F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606840 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACGGGATCCGGCTGGAGGACCGAGGCACGGCACGGTGGGCCGAGCACAGAACTACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           566 tacgggatccggctggaggaccgaggcacgggcacggtgggccgagcacagaactaccag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.7%; Score 403; DB 21; Length 432; 98.6%; Pred. No. 7e-80; ive 0; Mismatches 5; Indels
ity sequence stop: 183.
Location/Qualifiers
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BE391975.1 GI:9337340
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Matches 417; Conservative
  High quality
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BE391975
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Eukaryota; Metazoa: Chordata; Craniata: Vertebrata; Euteleostomi;
Eukaryota; Metazoa: Chordata; Craniata: Vertebrata; Euteleostomi;
Mammalia: Eutherla: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 432)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC.

National Institutes of Health, Mammalian Gene Collection (MGC)
Upublished (1999)
Upublished (1990)
Upublis
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2822396.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822396 5',
mRA sequence.
AW250708
AW250708.1 GI:6593701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 TCGAGCACTTCCAGGCGCCGCTGGTCCGCTTCTTCCTGGAGGAGGCGTGGTGCGGCGGG 133
                                                                                                                                                                                468 atgecaagececteaegeteagggaggtegaggtgtttaaaageteeeaggagateeeagg 527
                                                                                                                                     Gaps
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                                                                                                                                     ä
                                                                                                                                     6; Indels
                                                                                          Length
                                                                                      Score 411; DB 13;
Pred. No. 1.2e-81;
0; Mismatches 6;
  73
    φ
  142
                                                                                      Query Match 33.4%;
Best Local Similarity 98.4%;
Matches 425; Conservative
    O
  143
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RESULT 10 AW250708 LOCUS

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DEFINITION

ACCESSION

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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744

309

864

804

429

924

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EST 13-JUL-2000 musculus cDNA clone IMAGE:3495186 5',
                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 654)

NIH-MCC http://www.ncbi.nlm.nih.gov/MCC/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550

Enail: Robert Strausbergenih.gov

Tissue Procurement: Gallbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="Index: 349186"
/clone="Index: 349186"
/clone=lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell Onigin."
/lab_host="Onigin."
/lab_host="Onigin."
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall;
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall;
/lab_rary constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

a 175 c 181 g 119 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94 ggaggacgaggactgcgaggacggcgaggccgccgcgcgagggacgcgggacgcagggga 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAGGACGAGAGCGAGGAGGACGCGAGCATGGCCAGGCGGATACGACCGATGAGGA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8545 row: f column: 19
High quality sequence stop: 552.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 GACAAGGTACCGAAACTGGCGTGCTATGCAGGACATGCAAAGATACCGGCACAACTACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ggatetggtggaacgagaetgcaatggggacacgccaaacetgagtttetacagaaatga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.7%; Score 390.4; DB 34; Length 654; 78.4%; Pred. No. 4.6e-77; Live 0; Mismatches 131; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. 654
/organism="Mus musculus"
/strain="C2ECH II (feral)"
/db_xref="taxon:10090"
            BE282484 654 bp mRNA
601103075F1 NCI_CGAP_Lu29 Mus
                                                                                                                               BE282484.1 GI:9158085
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                                                              mRNA sequence.
BE282484
                                                                                                                                                                                          house mouse.
Mus musculus
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(Ab_zref="Homo sapiens")

(Ab_zref="Homo sapiens")

(Ab_zref="Homo sapiens")

(clone="lib="NIH_MGC_44"

(clone="lib="NIH_MGC_44")

(lab_nost="DH10B" (bhage=resistant)"

//assue=_yppe="endometrium, adenocarcinoma cell line"

//assue=_yppe="endometrium, adenocar
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Contact: Robert Strausberg, Ph.D.
Thel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tgggaggaggacgaggaggatgcggaggac-gcggaggacgaggactgcgaggacg-gcg 119
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                                                                                                                                               Tissue Procurement: ATCC CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can lette://image.lnl.gov consortium/LLNL at: http://image.lnl.gov consortium/LLNL at: High quality sequence start: 77 High quality sequence start: 77 High quality sequence stop: 548.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.3%; Score 398; DB 35;
97.7%; Pred. No. 9.3e-79;
11ve 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 97.7
Matches 467; Conservative
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BE282484
      TITLE
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BE274933 886 bp mRNA EST 13-JUL-2000 601123054F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3347100 5',
                                                                                                                                                                                                                                                                                                                                           303 GAAAATAGATCCGCTTCCTGCCCAACGGCTGTTTCATTGAGGACATTCTTCAGAACTGGA 362
was constructed by Dr. Claudio Schneider (LNCIB-Area Science Park, Trieste, Italy). " 109 c 138 g 55 t
                                                                                                                                                                                   4 ecceaecargeaceacccceacrg-ceacrccaccrggaggaggacgaggargeagg 62
                                                                                                                                                      27 gccgagcatggacgaccccgactgncgactccacctgggaggaggacgaggatgcgg
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                                                                                          Length 400;
                                                                                                                       3; Indels
                                                                                       Score 381.2; DB 13;
Pred. No. 5e-75;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/clone="liMxGE:347100"
/clone=lib=WHH_MGC_20"
/tissue_type="melanotic melanoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .886
/organism="Homo sapiens"
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                                                                                        30.9%;
Best Local Similarity 99.0%;
Matches 394; Conservative
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AUTHORS
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Bukaryota; Metazoa; Chordata; Catarrhin1; Hominidae; Homo.

1. (bases 1 to 400)

1. (bases 1 to 400)

1. (bases 1 to 400)

1. Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.

Mashu-NCI human EST Project

1. Unpublished (1997)

Contact: Wilson RK

Washighton University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson, wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@fange.llnl.gov) for further information.

Seq primer: -40RP from Gibco.

High quality sequence stop: 383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissum_type="frontal lobe"
//dev_stage="5 months post-conception"
//dev_stage="5 months post-conception"
//dev_bost="DHIGH"
//dev_forgan: brain; Vector: pBluescript SK (Stratagene);
Site=1: SstI; Site=2: XhoI; Double-stranded CDNA was
prepared from human fetal brain tissue. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
                                                                                                                                                                                                                                                                                                                                             A1816230 400 bp mRNA EST 09-JUL-1999 au45h07.yl Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2517757 5' similar to contains element MSR1 repetitive
                                                                                                            coggetggaggaccgaggcacggtgggccgagcacagaactaccagaagggtt 633
                                                                                                                                   634 -cagaactgaactggcgcagcacaacaactccgcatcacacgcatcctcaagtcgcc 692
                                                                               434 CAAGGAAGTCAGAGGGTCTTGTCCGGGCCTATGAGCTCATGCTGGGGCTTCTATGGGAT 493
                                                                                                                                                                                                      554 ACACAACCICAAAAGCCACAGACACAACAATCIGCGIATTACACGCAICCICAAGICGCI 613
    ccaggagatccaggagcgcttgtccgggcctacgagctcatgctgggcttctacgggat
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/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone=linasp:2517757"

/clone=lib="Schneider fetal brain 00004"

/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                            element; , mRNA sequence.
AI816230
AI816230.1 GI:5431776
                                                                                                                                                                                                                                       gtgtgagctgag 704
                                                                                                                                                                                                                                                                       614 GGGCGAGCTGGG 625
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                                                                                                                                                                               16;
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCAGGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
246 c. 287 g. 177 t.
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                                                                                                                                                                                                                                                                          GAGT----GGAGGAGCGTGGGCGGGCGTGCCCAGTCGTTCAGTCCAGAATGACAGTGT-C 193
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                                                                                                                                                                              27;
                                                                                                                                                        Length 886;
                                                                                                                                                                              Indels
                                                                                                                                                        DB 34;
                                                                                                                                                       Score 363.4; DB 34;
Pred. No. 4.9e-71;
0; Mismatches 131;
                                                                                                                                                       Query Match 29.5%;
Best Local Similarity 79.9%;
Matches 629; Conservative
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Best Local
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Lough Mus musculus.

Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Musmalia; Eutheria: Rodentia; Sciurognathi; Muridae: Murinae; Mus. 1 (bases 1 to 590)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Tan,F., Martin,J., Morre,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

The MashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashIngton University School of MedicineP
WashIngton University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
Eax: 314 286 1810
Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:969331
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AI115047 590 bp mRNA EST 02-SEP-1998 u141f12.yl Sugano mouse embryo mewa Mus musculus cDNA clone IMAGE:1885007 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.8%; Score 355.4; DB 8; Length 76.7%; Pred. No. 2.9e-69; ive 0; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone_lib="Sugano mouse embryo mewa"
/dev_stage="embryo, 14 dpc"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seg primer: custom primer used
High quality sequence stop: 531.
Location/Qualifiers
1..590
                                                           AI115047
AI115047.1 GI:3515371
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Matches 434; Conservative
                                                                                                                               house mouse.
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145 ACGCCCAAGCCTGTTCCAGTCTAGGATGACAAGGTACCGAAACTGGCGTGCTATGCAGGA 204
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AW538283.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           National Institute on Aging/National Institutes of Health 33 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, t Email: cdnaelgsun.grc.nia.nih.gov Plate: C0105 row: F column: 08 Plate: C105 row: F column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome-wide expression profiling of mid-gestation placenta embryo using a 15,000 mouse developmental cDNA microarray Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
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III, Becker,K.G. and Ko,M.S.H.
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/note-"Vector: pSPORT1 (Gibco/BRL Life Technology);
Site_1: SalI; Site_2: NotI; Total RNAs were extracted from
5 EPC. The double-stranded cDNA was synthesized by
                                                                                                                                                                                                                                                 /sex="unknown"
/dev_stage="7.5dpc Embryo"
/lab_host="DH10B"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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                                                                            1 (bases 1 to 403)
Bonaldo, M.F., Lenno
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                                                                              Lennon, G. and Soares, M.B.
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                                                                                                                                                                                                 Email: msoares@blue.weeg.uiowa.edu

The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonatide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
non-normalized atrium at 16.5 dpc library cDNA Library Preparation:
M.B. Soares Lab Clone distribution: clones will be available
through Research Genetics (www.resgen.com)
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//lab_host="DH1UB (Life Technologies)"
//lab_host="DH1UB (Life Technologies)"
//lab_host="Wetotor: pT773D-Pac (Pharmacia) with a modified note="Wetotor: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-AAO library is a non-normalized library constructed from 10 library is a non-normalized library constructed from 10 dpc rat atrium. The tag is a string of 5 nucleotides present between the Not I site and the oligo-dT track. The library was constructed as described by Bonaldo, The library was constructed by Bonaldo, The library was constructed by Bona
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Tissue provided by Jim Lin, Department of Biology,
University of Iowa."
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-AAO-w1-g-01-0-UI"
/clone_lib="UI-R-AAO"
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Pred. No. 4.5e-75;
0; Mismatches 10
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gaacagccacagccacaacaacctgcgtattacacgcatcctcaagtcactgggtgagct 788
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Koehrer, K., Beyer, A., N
EST (Koehrer, et al.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Project.
No sl sequence available.
This clone (DKFZp762B143) is available at the Please contact the RZPD: Ressourcenzentrum, Please contact the RZPD: GERMANY; Email: clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \tt DKFZp762B143\_r1 762 (synonym: hmel2) Homo sapiens cDNA clone \tt DKFZp762B143 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Email s.wiemann@dkfz- heidelberg.de; sequenced by BMFZ (Biomedical Research Center at the Charite, Berlin/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Am Klopferspitz 18a D-82152 Martinsried, Ge
This is the 5' sequence of the clone insert
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/clone_lib="762 (synonym: hmel2)"
/tissue_type="melanoma (MeWo cell
/dev_stage="adult"
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Ressourcenzentrum, Heubnerweg 6, 14059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="BAA78219.1"
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/t=anslation="MROTYTETDDKGRLLAWOLGKKNKQRCKILTKETSLHPLPTPST
TIPPPLRNHFCPRFSHRRVHTQTRRHAHTTSMAVAGGQAGSIRGADVKSMRNGIARDV
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/gene="DRHN2"
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/gene="DRHN2"
                                                                                               complement(9467. .10768)
/gene="U2"
                                                                                                                                       complement(9467.
/gene="U2"
                                                                                                                                                                             /translation="mrraprraidLstdprpisymqirtrtrtdmptrphradchyse
sihthekihtrkytqenthtqkythkkihtqkkihthkkihtqknthtqknthtqknt
htkkythtkkythkkihthkkihtkknhfiyalfsqc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_1d="BAA78220.1"
/db_xref="GI:4995987"
/translation="MALAAVLSFLRRLLVCPSAALPSASLSLSRAPSFFRSHRAPAPG
CTFAFKLHAIHPHTLARSLGGGGGGIPGAGRTGDTRGRLGPVREGRFFHAPLAVARVL
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/gene="LJ1"
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RRCLTDRKYVFFLLCGVSNTERKHIVCDCVHSPILFLIGLKAGRDTVTRTYTHPTHTR
RRIDISTAVLLFLFLRLRTPHFFFFVLYFEILVMIFLRSCLWPYIASLRLRRGV"
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/protein_id="BAA78217.1"
/db_xref="GI:4995984"
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/gene="DR7"
/function="transforming activity"
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/db_xref="GI:4995985"
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/protein_id="BAA78222.1"
/db_xref="GI:4995989"
                                                                                                                                                                                                                                       /protein_id="BAA78221.1"
/db_xref="GI:4995988"
                                                                                                                                                                                                                                                                                                                                                                             /gene="Ul"
                                       /codon_start=
                                                                               /note-"92% identical to
                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                         note="25.6% identical to Ul
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JOURNAL MEDLINE REFERENCE AUTHORS

TITLE

Intragenomic linear amplification of human herpesvirus 6B oriLyt suggests acquisition of oriLyt by transposition J. Virol. 69 (1), 589-596 (1995)

Stamey, F.R., Dominguez, G., Black, J.B., Pellett, P.E.

Dambaugh, T.R.

(bases 64106 to 84963)

ogy 195 (2),

521-531 (1993)

REFERENCE

95074921 3 (base

(bases 64106 to 84963; 106012 to 126166)

JOURNAL MEDLINE

ACCESSION

AF157706 16Ž114 bp DNA VRL Human herpesvirus 6B strain 229, complete genome. AF157706 L13162 L14772 L16947 AF157706.1 GI:5733510

20-SEP-1999

LOCUS

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VERSION KEYWORDS

SOURCE

ORGANISM

Human herpesvirus 6B.
Human herpesvirus 6B
Viruses; dsDNA viruses,

no RNA stage; Herpesviridae;

REFERENCE

AUTHORS

1 (bases 19696 to 22886)
1 (bases 19696 to 22886)
Pellett, P.E., Sanchez-Martinez, D., Dominguez, G., Black, J.B.,
Anton, E., Greenamoyer, C. and Dambaugh, T.R.
Antongly immunoreactive virion protein of human herpesvirus 6
A strongly immunoreactive virion protein and characterization of the
variant B strain 229: identification and characterization of the
gene and mapping of a variant-specific monoclonal antibody reacti

reactive

TITLE

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RESULT 12
AF157706/c
                                                                                                                                                                        Db 129065 TCCAGCAGAGCCTCCAGCAGGGCCTCCAGCAGGGCCTCCAGCAGCCTCCAGCAGAGCC
                                                                                    Db 129005 TCCAGCAGAGCC 128994
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                                                                                                                                                                                                                                                                                                                                             TCCAGCAGGGCCTCCAGCAGAGCCTCCAGCAGAGCTTCCAGCAGAGCCTCCAGCAGGGCC 129126
                                                                                                                                                                                                                                                                                                                                                                     gccagccgagagcccatcggagaccccaggccccgcccggcaggacctgcaggggacga 1811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     gccagccgagagcccatcggagaccccaggcccggcaggacctacaagggatga 1751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gccagccgagagcccatcggagaccccaggccccgcccggcaggacctgcaggggacga 1691
                                                                                                                                                                                                     gccagccgagagcccatcggagaccccaggcccagcccggcaggacctacaagggatga 1931
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                                                                                                                                                                                                                                                                                       204;
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      Seguence
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/gene="U3"
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xqlsphmveremsavscgastvyrrdcedtlrdgdagvdts"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPRGAFFEFAVPRRAEKRWRLIPGGGVAVVIGRFFGRGVTLPLLRRQRVLMDQVGRVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGITQAELAKLSRGYGCCPGMDLTVIGVTIFAEVSALVLVGECGEIYAFNGVFDDALY
RLAEDAFGLWKHGLRRFEPVYGSKCLMETGASFFGGNSGVDDALAFAVSFDKALVPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRCDAAVPEVKWTAFVRTLVARPLSADDVRDFVSTFAHCRLALSWPVGAELRFATSDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPVTLPLSFFFFFILLILSRIPHRKKMFCRSPFLGISSWSLASAALCPSSCSFSAGRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MCSQFCGRSVHFHFRGRREYVDSTLFVSNSCSVLNVIVDVYVR/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.8%;
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Pred. No. 3.6e-07;
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                      Cempon son
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GA 30333,
9 (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GA 30333, US.
8 (bases 64
Pellett, P.E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Restriction endonuclease mapping and molecular cloning of the human herpesvirus 6 variant B strain Z29 genome Arch. Virol. 141 (2), 367–379 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence updated by submitter on Aug 16, 1999 this sequence g1:305397.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission submitted (02-OCT-1993) Control and Prevention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission submitted (26-JUL-1993) Control and Prevention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human herpesvirus 6B genome sequence: with human herpesvirus 6A
J. Vicol. 73 (10), 8040-8052 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (10-JUN-1999) Herpesvirus Section, Control and Prevention, 1600 Clifton Road, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                                                   /rpt_unit=tarsyc 583. .3988
                                                                                                                                                                                                                                                                                                                                        1. .162114
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                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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join(583. .841,955.
                                                                                                                                                                                                                                                                  .8793
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                                                                                                               family"
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B1; B2"

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gene
                                                                     SgS
polyA_signal
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Best Local Similarity Matches 207; Conserv Conservative 4.4%; 0 Score 101.4; DB 7 Mismatches 176; DB 72; Length 162114; Indels 0; Gaps

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129440

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Š g 129320 CTAGCAAAGCTTCCAGCAGAGCCTCCAGCAGAGCCTCCAGCAGGGCCCT

δÃ 밁 129260 CCAGCAGGGCCTCCAGCAGGGCCTCCAGCAGAGCCTCCAGCAGAGCCT gcaggggacgagccagccgagagacccatcggagacacccaggcccagcccagcccggcaggacct 1920

acaagggatgagccagccaaggc 1943

밁 Š 129200 CCAGCAGAGCTTCCAGCAGAGCC 129178

LOCUS DEFINITION ACCESSION RESULT 13 AF015297 KEYWORDS VERSION ORGANISM Human he AF015297 Human herpesvirus 6 (strain Uganda-1102). Human herpesvirus 6 (strain Uganda-1102) Viruses; dsDNA viruses, no RNA stage; Her AF015297.1 AF015297 Betaherpesvirinae; Roseolovirus 297 4742 bp mRNA VRL 2/-AUG-1997 herpesvirus 6 (strain Uganda-1102) IE2hom mRNA, complete cds. GI:2343282

Herpesviridae;

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CCAGCAGGGCCTCCAGGGGCCTCCAGCAGGGCCTCCAGCAGCTTCCAGCAGAGTCT 129321 CCGGCAGGGCCTCCAGCAGAGCTTCCAGCAGAGTCTCTAGCAGAGCTTCCAGCAGGGCCT 129381 LDSSLYVCCGYGEKLQPVGFVSSYLTHSPLDTLRVLLVGRDGAVYVHHMRAARLCRLA SNYTESARRGLQRDVYAYEEDLELPDRRWGCGTNVTLEDVIAAAADEHDLLTVGGLCQ THAGVSCELLETVRDDWTAVPGVRWTLTVARAQYRLWPDARRQLRLHLYAGHPLGPWI VCAVLSRERETQTPSPPIGSGGVILGNVPTPGPREVETAWVIVTVAGPLLSFWPDNGK ICRLANSFAALWRMGPRAMRGHWTYSAPGRHLPGDAWPLCEHVRPPVGKLPRQRAYLD 12926 0 JOURNAL REFERENCE AUTHORS TITLE FEATURES BASE COUNT ORIGIN JOURNAL gene Sg source

REFERENCE AUTHORS TITLE Soergel,A., Schiewe,U., Fleckenstein,B. and Neipel,F. Identification of an human herpesvirus-6 transcription unit homologous to the immediate early 2 gene of human cytomegalovirus Submitted (21-JUL-1997) Institut fuer Klinische und Molekulare Virologie, Universitaet Erlangen-Nuernberg, Schlossgarten 4, Direct Submission Soergel, A., Schiewe, U., Fleckenstein, B. and Neipel, F Unpublished evidence for early/late gene Erlangen D-91054, Germany (bases 1 to 4742) pergel,A., Schiewe,U., (bases 1 to 4742) 1772 a SENTING DEVICE THE PERSONGEY NETWONDER OF PRETTURE OF THE TURE OF THE SENTING OF /protein_id="AAB67722.1"
/protein_id="AAB67722.1"
/protein_id="AB67722.1"
/db_xref="GI:2343283"
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SNESGSTQVRFASELPNQLLQPMYTSHNQNANLQNNFTSLPYQPTRDIESSYRE cytomegalovirus" TMIIYAATPIDFVGAVKTCNKYAKDNPKEIVLRVCSIIDGDNPISIYNPISKEFKSKF FEYKOIPKKPCNEKNLKEAVYDICCNGLSNNAAIIMYFTRSKKVAOIIKIMOKELMIR PNITVSEAFKMNHAPPKYYDKDEIKRFIOLOKOGPOELWDKFENNTTHDLFSRHSDVK /product-"IE2hom" /gene="ie2hom" /organism="Human herpesvirus 6 (strain Uganda-1102)" /db_xref="taxon:10370" 1. .4742 Location/Qualifiers KRISGAQKTESEVSEPDDLCYRDYVRLKERKVSEKFKIHRGRVATKDFQKLFRNTMRA 1134 c .4698 'ie2hom" φ the immediate-early 2 protein of human

멍 밁 å Matches Query Match 4.0%; Best Local Similarity 52.8%; 1561 cccaaagaaggtacccctgggagcccatcggagaccccagcccagcccagcaggacct 1620 1681 gcaggggacgagccagcccgagagacccatcggagaccccaggcccagcccggcaggacct 2522 2462 CCAGCAGAGCCTCCAGCAGGGATTCTAGCAGAGCCTCCAGTAGAGCCTCCAGCAGGGCCT 2582 CTAGCAGGGCCTCAAGCAAAGCCTCCAGCAGAGCCTCCAGCAGGGATTCTAGCAGAGCCT CAAGCAAAGCCTCCAGCAGAGCCTCCAGCAGAGCCTCCAGCAGAGCCTCCAGCAGGGATT 199; Conservative 0 Score 92.2; DB 72 Pred. No. 6.9e-05; Mismatches DB 72; 178; Length 4742; Indels 0 Gaps 2521 2641 1740 2581 0

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Human herpesvirus 6B strain Z29, complete genome.
AF157706 L13162 L14772 L16947
AF157706.1 GI:5733510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lindquester G.J., O'Brian, J.J., Anton, E.D., Greenamoyer, C.A., Pellett, P.E. and Dambaugh, T.R. Genetic content of a 20,9 kb segment of human herpesvirus 6B strain 229 spanning the homologs of human herpesvirus 6A genes U40-57 and containing the origin of DNA replication Arch. Virol. 142 (1), 103-123 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pellett, P.E., Sanchez-Martinez, D., Dominguez, G., Black, J.B., Anton, E., Greenamoyer, C. and Dambaugh, T.R. A strongly immunoreactive virion protein of human herpesvirus 6 variant B strain 229: identification and characterization of the gene and mapping of a variant-specific monoclonal antibody reactive gene and mapping of a variant-specific monoclonal antibody reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Intragenomic linear amplification of human herpesvirus 6B oriLyt suggests acquisition of oriLyt by transposition J. Yirol. 69 (1), 589-596 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human herpesvirus 6B
Viruses; dsDNA viruses,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Restriction endonuclease mapping and molecular cloning of the human herpesvirus 6 variant B strain Z29 genome Arch. Virol. 141 (2), 367-379 (1996)
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Lindquester,G.J., Inoue,N., Allen,R.D., Castelli,J.W.,
Dambaugh,T.R., O'Brian,J.J., Danovich,R.M., Frenkel,N.
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Lindquester,G.J., Greenamoyer,C.A., Anton,E.D., O'Brian,J.J.,
Pellett,P.E. and Dambaugh,T.R.
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1 (bases 19696 to 22886)
9 (bases 1 to 162114)
Pellett, P.E., Domingue
                                                                                                                                            GA 30333, USA
8 (bases 64106 to
                                                                                                                                                                           Direct Submission
Direct Submission
Submitted (26-UTL-1993) Herpesvirus Section, Centers for Submitted (26-UTL-1993) Herpesvirus Section, Centers for Submitted and Prevention, 1600 Clifton Road, Mailstop G18,
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                                                                                    Direct Submission Submitted (02-OCT-1993)
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Virol. 73 (10), 8040-8052 (1999)
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      Dominguez,G.,
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                                                                   Herpesvirus Section, Centers for 1600 Clifton Road, Mailstop G18,
      Dambaugh, T.R.,
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Submitted (10-JUN-1999) Herpesvirus Section, Centers
Control and Prevention, 1600 Clifton Road, Mailstop G
GA 30333, USA
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join(583. .841,955. .2975)
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'evidence=not_experimenta.
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                                                                                             9999ac9a9ccagccaagaccccatcggagaccccaggccccagcccggcaggacctaca 1683
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/gene="B4"
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Thagvscelletvrdpwtavpgvrmtltvaraqyrlwpdarrglrhhyaghelgruf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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join(5027. .5330,6329. .7203)
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3938. .3942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Soergel,A., Schiewe,U., Fleckenstell, B. and Miller and Internation of an human herpesvirus of transcription unit homologous to the immediate-early 2 gene of human cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (21-JUL-1997) Institut fuer Klinische und Molekulare Virologie, Universitaet Erlangen-Nuernberg, Schlossgarten 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human herpesvirus 6 (strain Uganda-1102).
Human herpesvirus 6 (strain Uganda-1102)
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human herpesvirus
AF015297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Erlangen D-91054, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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CSDRSADILPYEHYTYPPYEQONPDPRMNYKDFTQLINKFNFESYDYSMAFGFDSTHY
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KIYOTDVIPLPKEALTANGSNRDVDIQKYKKAHIRCRSVQKKKERSSQTNKHDENHAS
SRSDLKERKSNENEDKAVTKAADFSKLNPLLSPLPLTPEPALDFADHTDKFYSTPEFN
QIQQNLHRSKTSLQDTVPISKHTPRAPTKDNSYKKHHDSKDNYPKMKHSPGRTTSKKN
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                                                                                                                                                                                                                                                                                                                                                                                /gene-
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                                                                                                                                                                                                                                                                                           codon_start=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecular cloning of the high affinity calcium-binding protein (calreticulin) of skeletal muscle sarcoplasmic reticulum J. Biol. Chem. 264, 21522-21528 (1989)
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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Rabbit (neonatal) skeletal muscle sarcoplasmic reticulum, cDNA to
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nilarity 59.9%;
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/Protein_id="AAA31188.1"
//LTANS14 tion="MILPVPLLIGILGLAAAEPVVYFKEQFLDGDGWTERWIESKHKS
//LTANS14 tion="MILPVPLLIGILGLAAAEPVVYFKEQFLDGDGWTERWIESKHKS
//LTANS14 tion="MILPVPLLIGILGLAAAEPVVYFKEQFLDGDGWTERWIKSKYVLINKD
DEGGCYVKLEFAGLDGKDMHGDSEYNIMFGPDICGPGTKKYWIITNYKGKWYLINKD
IDCGGGCYVKLEFAGLDGKDMHGDSEYNIMFGPDICGPGTKKYWIITNYKKIKDPDASKFED
IRCKDDEFTHLYTLIVREDWTYEVKINSQVESGSLEDDWDFLPFKKIKDPDASKFED
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/db_xref="taxon:9986"
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                                                    Score 65.2; DB:
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ICP0; ICP27; ICP34.5; RL1; RL2; Syn-associated membrane
glycoprotein; UL53; UL54; UL55; UL56; Vmw118; Vmw63; long repeat
region; long unique region; neurovirulence factor; transcriptional
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Whitton,J.L., Rixon,F.J., Easton,A.J. and Clements,J.B. Immediate-early mRNA-2 of herpes simplex viruses types 1 and unspliced: conserved sequences around the 5' and 3' termini correspond to transcription regulatory signals Nucleic Acids Res. 11 (18), 6271-6287 (1983)
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                                                                                                      /product."Syn-associated membrane glycoprotein"
/protein_id="BAA01268.1"
/db_xref="G1:221787"
/translation="DevifixHreaigvivgcelllerevalglivgTalisrgacaif
/translation="DevifixHreaigvivgcelllerevalglivgTalisrgacaif
HPLFLITTWCFVSIIALTELYFILRRGSAPKNAEPAAPRGRSKGWSGVCGRCCSIIL
SGIAVRLCYIAVVAGVVLVALRYEQEIQRRLFDL"
                                                                                                                                                                                                                                                                                       /organism="human herpesvirus
/isolate="HG52"
/db_xref="taxon:10310"
                                                                                           460.
                                                                                                                                                                                                                                                                    /clone="f, p and g"
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note="UL54 ORF"
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                                   CTCTGAGGTAGAGAAAATTGCCCTTAACCTTGAGGAGTGTGCCCTTAGCCCTATCAGC--
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                                                                                   AAGGAAGTTGGAGGGGAACAGGCAGGAGCAGGTCCCCAGGGGAGGCAGATCCCCCAGGGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF157706 162114 bp DNA VRL
Human herpesvirus 6B strain Z29, complete genome
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AF157706.1 GI:5733510
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Virology 195 (2), 521-531 (1993)
93331710
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Betaherpesvirinae; Roseolovirus.
1 (bases 19696 to 22886)
                                                                                                                                          Lindquester,G.J., Greenamoyer,C.A., Anton,E.D., O'Brian,J.J., pellett,P.E. and Dambaugh,T.R. Comparison of a 20 kb region of human herpesvirus 68 with other human beta herpesviruses reveals conserved replication genes an adjacent divergent open reading frames arch. Virol. 142 (1), 193-204 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 (bases 64106 to 84963; 106012 to 126166)
Lindquester,G.J., Inoue,N., Allen,R.D., Castelli,J.W.,
Dambaugh,T.R., O'Brian,J.J., Danovich,R.M., Frenkel,N.
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J. Virol. 73 (10), 8040-8052
                                                                                                                                                                                                                                                                                         Lindquester.G.J., O'Brian,J.J., Anton,E.D., Greenamoyer.C.A., Pellett,P.E. and Dambaugh,T.R. Genetic content of a 20.9 kb segment of human herpesvirus 6B strain Z29 spanning the homologs of human herpesvirus 6A genes U40-57 and containing the origin of DNA replication Arch. Virol. 142 (1), 103-123 (1997)
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                                     n herpesvirus 6B genome sequence:
human herpesvirus 6A
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/strain="229"
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/product="DR1"
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                                                 /translation="MSRVFSCYLRACYCAGLCCWYCMGYICGDCQRWWRRRCARWGRV
/translation="MSRVFSCYLRACYCAGLCCWYCMGYICGDCQRWWRRRCARWGRV
GPRYLDGGAMRYRSGDGARSYSRTCETERAPSAARSPYISPPFYLVSSSSSSSSSSSCSSAC
SSRVPSPPPSPHAASHAYCAEGGRDLPMHGADGDADBGTDGTLLEKGGADEGAGGNAT
GCPEDTHGFARSPGDLMGEMNGDLGDEGETGEGGDNGEGE"
                                                                                                                                                                                                /evidence=not_experimental complement(2723. .3325) /gene="DR3"
                                                                                                                                                                                                                                                                                         SPPSPVSPSSPRSPFISPIRSPGLRAKPWVSSGHPVAFPPAPSSAPPFSKRVPSVPSS
ASPSAPCIGRSRPPSAQTA"
               /gene="B1"
                                                                                                                          /protein_id="AAD49618.1"
/db_xref="GI:5733515"
evidence-not_experimental
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/note="DR1; B1; B2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1-
                                                                                                                                                                                                               /evidence=not_experimental
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                  5.2%;
                  Score 122;
                                                                                                           .9492)
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                    DΒ
                      72;
                      Length 162114;
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UL8"

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Db 129677
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VERSION
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ORGANISM
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kosuge,H., Isegawa,Y. and Yamanishi,K. Nucleotide sequence analysis of a 30-kilobase-pair region of human herpesvirus-6B (HHV-6B) genome and strain-specific variations in major immediate-early genes

Virus Res. 52 (1), 1-14 (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Betaherpesvirinae; Roseolovirus.
1 (bases 1 to 30752)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human
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                                                                                                                                                                                                                                                                                                                     Kosuge,H., Isegawa,Y. and Yamanishi,K.
Direct Submission
Submitted (07-MAR-1997) Virology, Research Institute for Microbial
Submitted (07-MAR-1997) Virology, Research Suita, Osaka 565, Japan
Diseases, Osaka University, 3-1 Yamada-oka, Suita, Osaka 565, Japan
Diseases, Osaka University, 3-1 Yamada-oka, Suita, Osaka 565, Japan
Diseases, Osaka University, 3-1 Yamada-oka, Suita, Osaka 565, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30752 bp DNA VRL 04-MAY-2000
3Virus 6 serotype B putative major immediate-early
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0; Mismatches 195;
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ERSIQITQCKQDLSIYMPVISDIAERALGAVACKTKELEDLCESVIVIDEAGVILRHI
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FYKRASYIRNPMNEIETTRLEIGHNEVKNYFRSLHEQVEVTNRNNLFVFPVFVFIK
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FYKRASYIRNPMNEIETTRLEIGHNEVKNYFRSLHEQVEVTNRNNLFFTNATH
FYKRASYIRNPMNEIETTRLEIGHNEVKNYFRSLHEQVEVTNRNNLFFTNATH
FYKRASYIRNPMNEIETTRLEIGHNEVKNYFRSLHEQVEVTNRNNLFFTNATH
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FYKRASYIRNPMNEIETTRLEIGHNEVKNYFRSLHEQVEVTNRNNLFFTNATH
FYKRASYIRNPMNEIETTRLEIGHNEVKNYFRSLHEQVEVTNRNNLFTNATH
FYKRASYIRNPMNEIETTRLEIGHNEN
FYKRASYIRNPMNEITTRLEIGHNEVKNYFRSLHER
FYKRASYIRNPMNEITTRLEIGHNEN
FYKRASYIRNPM
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/translation="LOSVFAFLHEKIFGVYKOVLVOLCEYIGPDLWPFGNERSVSFIG
YPNUMLLSVSDLERKVPDTTYICREILSFCGLAPILGPRGRHAIPVIRELSVSMPGSE
YPNUMLSVSDLERKVPDTTYICREILSFCGLAPILGPRGRHAIPVIRELSVSMPGAFU
TSLQRERENSQYVSSESLCFOOTGPEDTHLFFSDSDMYVTTLPDCLILLLKEMRWLLVRD
PCFDENATEIELLKFMSRLOHRSYALFDAVIEWLDAVIEWLDAVIEWLS
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PCFDENATEIELLKFMSRLOHRSYALFDAVIEWLDAVIEWLS
PCFDENATEIELLKFMSRLOHRSYALFDAVIEWLS
PCFDENATEIELLKFMSRLOHRS
PCFDENATEIELLKFMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LHVFYLTCDGKDSHVVMPLLQTAVENCWEKITEIKQRPAFQCKEISRCGFVFYARFFL
SSGLSQSKEAHWTVTASKYLSACIRANKTGLCFASITYVFQDMMCVFIANRYNVSYWI
EEFDPNDYCLEYHEGLLDCSRYTAVMSEDGQL/VRQARGIALTDKINFSYYILVTLRVL
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RRLHMKVDTPEEFMLGGLYFALENDLAGSTLHKLIARLVLFPVLSPVTKRSHNFINLSLE
KLVCTLRHLFFNEHASSEILHKVPPMIRLYNEMKNTHIEVLELYFNTKRSHNFINLSLE
SRQLQDSSLQVIQLATQFAQIFYSKNEDTSS"
complement(1974. .3962)
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/db_xref="GI:2769712"
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/gene="H75"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(1316.
/gene="H75"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRWVESKFEDVEQTEFIRWENRMLYEHIHLLHLN"
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BBRF2, EHV1 55, VZV 53, HSV1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /function="possible virion protein"
/note="similar to HHY6A U76, HCMV UL104, HVS gene 43,
/note="similar to HHY6A U76, HCMV UL104, HVS gene 43,
/note="similar to HHY6A U76, HCMV UL104, HVS UL104, HV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(1974. .3962)
/gene="H76"
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.3757. .6231
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/gene-"H77"
/function-"helicase, helicase-primase complex"
/functe-"similar to HHV6A U77, HCMV UL105, HVS ge
/note-"similar to YZV 55, HSV1 UL5"
BBLE4, EHY1 57, VZV 55, HSV1 UL5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAC40326.1"
/db_xref="GI:2769714"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
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                                                                                                                                                                                  .2065)
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UL7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene 42,
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ку29. .9384
∕gene="U1"
                                                                                                                                                           /protein_id="BAA78221.1"
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/td_xref="G1:4995988"
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HTKKYTHTKKYTHKKYTHTKKTHTHKKIHTKKHHFIYALFSQC"
                                                                                           complement(9467. .10768)
/gene="U2"
                                                                                                                                                                                                                                                                                                                                       /gene="U1"
8929. .938
                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/protein_id="BAA78222.1"
/db_xref="GI:4995989"
                                                  US22 gene family"
                                                                                                                                complement(9467.
/gene="U2"
                                                                                                                                                                                                                                                                                   "9-VHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RHLFDVIAAAADEHDLLTVGGLCQTHAGVSCELLETVRDPWTAVPGVRHTLTVARAQY
RLWFDKARQLKHHLTAGHFLGFWIVCAVLSRERETQTPSPF1GSGGVILGNVPTPGPR
EVETAWVITUTWRDRCTRSGPITARSAVWRTRSPPCGGWAAGHERTLDVFGPG*
complement(7236...7706)
//gene**DRHN2**
                                                                 /note="92% identical to U2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HHV-6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(8292. .8807)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAPRPGSPHLPPPKNGRGYGGGWRVV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="BAA78218.1"
/db_xref="GI:4995985"
/translation="MLAPTPRGVYIRGECGALSSSPDLCDSPCRVGIGRCYSNSARG
RRCLTDRKYVFFLLCGVSNTERKHIVCDCVHSDILFLLGLKAGRDTVTRTYTHFTHTR
RRIDISTAVLLFLFLRLRTPHFFFFVLYFEILVMIFLRSCLWPYIASLRLRRGV"
                                                                                                                                                                                                                                                                codon_start=1/
                                                                                                                                                                                                                                                                                           note="25.6% identical to U1 gene of strain U1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="LJ1"
/note="16.6% identical toLJ1 gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="LJ1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "9-VHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7928. .8662
/gene="DR8"
                                                                                                                                                                                                                                                                                                                                                                                              GLGLGLGLGL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="BAA78219.1"
/db_xref="GI:4995986"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(7236. .7706)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="BAA78217.1"
/db_xref="GI:4995984"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /function-"transforming activity"
/note-"42.2% identical to DR7 geno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="13.6% identical to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="ORF unique to HST /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="DRHN2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="mraarlcrlasnvtefarrglqrdpvayeedlelpdrrmcgtnv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'product="transactivator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene-"DR7"
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                                                                                                                                                                                                                                                                                                                                                                            .9384
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                                                                                                                                               .10768)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .8807)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DR8
                                                                   of.
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                                                                   strain U1102 of HHV-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ul102 of
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(bases 64106 to 84963;

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SOURCE
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VERSION
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AF157706/c
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DEFINITION
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Intragenomic linear amplification of human herpesvirus 6B oriLyt suggests acquisition of oriLyt by transposition
1. Virol. 69 (1), 589-596 (1995)
95074921
3 (bases 64106 to 84963: 106012 to 126166)
                                                                                                                                                                                                                         Pellett, P.E., Sanchez-Martinez, D., Dominguez, G., Black, J.B., Anton, E., Greenamoyer, C. and Dambaugh, T.R. A strongly immunoreactive virion protein of human herpesvirus 6 variant B strain Z29: identification and characterization of the gene and mapping of a variant-specific monoclonal antibody reactive
                                                                                                         Stamey, F.R., Pellett, P.E.
                                                                                                                                                                                 93331710
                                                                                                                                                                                                                                                                                                                                                                                                                       Human herpesvirus 6B.
Human herpesvirus 6B
                                                                                                                                                                                                Virology 195 (2), 521-531 (1993)
                                                                                                                                                                                                                                                                                                                                                        Viruses; dsDNA viruses, no RNA s
Betaherpesvirinae; Roseolovirus.
1 (bases 19696 to 22886)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF157706 162114 bp DNA VRL
Human herpesvirus 6B strain Z29, complete genome
AF157706 L13162 L14772 L16947
AF157706.1 GI:5733510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Legrence Componism
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AASLDGGAVVRLSDSFRAFLAMGVRKLFKNHRFPPGHLWTMQLPVTCVHAPVINLPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(10891. .12051)
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/gene="U3"
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                                                                                                                         Dominguez, G., Black, J.B., Dambaugh, T.R. and
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Pred. No. 3.4e-07;
0; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                             no RNA stage; Herpesviridae;
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g1:305397.
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Submitted (02-OCT-1993) Herpesvirus Section, Centers to Landau Submitted (02-OCT-1993) Herpesvirus Section Road, Mailstop (218, Atlanta, Centers)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lindquester,G.J., Greenamoyer,C.A., Anton,E.D., O'Brian,J.J., Pellett,P.E. and Dambaugh,T.R.
Comparison of a 20 kb region of human herpesvirus 6B with other human beta herpesviruses reveals conserved replication genes and adjacent divergent open reading frames
Arch. Virol. 142 (1), 193-204 (1997)
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Genetic content of a 20.9 kb segment of human herpesvirus 6B strain 229 spanning the homologs of human herpesvirus 6A genes U40-57 and containing the origin of DNA replication
Arch. Virol. 142 (1), 103-123 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence updated by submitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GA 30333, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (10-JUN-1999) Herpesvirus Section, Centers for Disease Control and Prevention, 1600 Clifton Road, Mailstop G18, Atlanta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pellett, P.E.,
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9 (bases 1 to 162114)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (26-JUL-1993) Herpesvirus Section, Centers for Control and Prevention, 1600 Clifton Road, Mailstop G18,
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J. Virol. 73 (10), 8040-8052 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dominguez,G., Dambaugh,T.R., Stamey,F.R., Dewhurst,S., Inoue,N. and Pellett,P.E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lindquester,G.J., Inoue,N., Allen,R.D., Castelli,J.W., Stamey,F.R., Dambaugh,T.R., O'Brian,J.J., Danovich,R.M., Frenkel,N. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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59. .
                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain-"229"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Human herpesvirus"
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                                                                                                                                                                                                                          rpt_unit=tarsyc
                                                                                                                                                                                                                                                     rpt_type=tandem
                                                                                                                                                                                                                                                                              'note="heterogeneous telomeric unit"
                                                                                                                                                                                                                                                                                                                                                                                     'note="variant B"
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                                                /codon_start=1
/product="DR1"
                                                                                                 gene="DR1"
                                                                                                                               oin(583.
                                                                                                                                                    note="US22 gene family"
protein_id="AAD49614.1"
/db_xref="GI:5733511"
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GLAAFYALWRLHLGSRSELSHPYLEWERTELYLTDRRRGWPCTHLLSGSESQRYSSSD AGDTWNAATEKAAGGKEEAERGGRQQATDRLASPHLTRGRRDCGRSLQGEEPSAAEDF /translation="MPLTARAGHTLHRLPLSHYMWILLGRHSLHHVHSYLRLBRGLRLPLHPREDENTHPSADSKLLPLPKPYKFLLRYRDCLTRDGWPADSSLWFDPKYHPSADSKLLPLGREGRETHLTSASSKLLTTLSASFORKVSBFPHCSGFBADPSLSWLTGSSFWLTLAPGRGSLFCHDVFORRUTTLSAFGKFLYLLQAPGGSLFCHDVFORRUTTLSHSVSLFLKTGLRQCBAIYRAPLWRVRPLPSLWTCRDPDTAFLPKLLARTARR /...e="US22 gene family; transactivator" join(5027. ..5330,6329. .7203) /gene="DR6" /translation="MSRVFSCVLRACVCAGLCCWVCMGVICGDCQRWWRRRCARWGRV GPRVLDGGAWRVRSGDGARSVSRTCETERAPSAARSPVYSPPFVLVSSSSSSSCSSAC SSRVPSPPPSPHAASHAVCAEGGRDLPMHGADGDADEGTDGTLLEKGGADEGAGGNAT /evidence=not_experimental complement(2723 ...3325) complement(2723. /gene="DR3" SPPSPVSPSSPRSPFISPIRSPGLRAKPWVSSGHPVAFPPAPSSAPPFSKRVPSVPSS ASPSAPCIGRSRPPSAQTA /translation="MQKNMKTKKTKKRGRKEGNTPETERRMEPARSRTSAIPSGLRRR SGPSTPLRPGPEVRHAPTWRTASATTADSHRISPPYTPSSRGRHIHTRGARTRTRETS GCPEDTHGFARSPGDLMGEMNGDLGDEGETGEGGDNGEGE" HGAWSSIPLSVPRPDPRVWVPPPHLLFPSPLPSITPVEDEPSARPRCPPGPAEEPSKC SPCPPCPSPDAPQSAVPRLSALSVPSPSTARVRFSLSSLSSSSSSSSSSSSSPSYSPSPL GYTEKGRYTTGDVPFSAHPESEEQTDGHHGRQESGHGDQRGGDGRGHRDDGARRHAND 3983. .3988 /note="DR1; B1; 3938. .3942 /note="DR1; B1; B2" APPTPPRSPLPPSPSPEHTRRLSPQRRRPQRQRKL" NAEINGVYARAVTRKTKRSETIDRLLLSVLPGHGPHASLRSHLRARSALRPPPDPPR" ETEPQQRGEHEDGEQTDSGREEDAQESEVARRDEKGTEQGGSGRSCGRATQTYGGRGE lrlgslillsglrlplrppsgsgeaarkpgyekeegrgrattasataatsprrptrpr ARCRPLLDELCGEGGWLPFAFLTASPHVCLILTEGGPVLALDLNDTSLWRIADDLELL /evidence-not_experimental /note="DR1; /evidence=not_experimental /evidence=not_experimental 3912. .3917 /note="DR1; B1; B2" translation="MQPMTKKKHTTASKRSPARPPSLSPPLESRRRVGGKSPERLHGN/ /db_xref="GI:5733513" /protein_id="AAD49616.1" /product="B2" /codon_start=1 /gene="B; evidence-not_experimental /gene="B2" /protein_id="AAD49617.1" /db_xref="GI:5733514" codon_start=1 /evidence=not_experimental /protein_id="AAD49618.1" /db_xref="GI:5733515" /codon_start=1 /gene="DR3" 'evidence-not_experimental B1; B2" B2 " . 3325)

/translation="MTTRHTQTRDGRIAIRRDGARLAHARARARFEWLLLARGRPSKL /GYTSRHRGERIHLPWPRYWCLELHPDPYRDARSATVWGHRWGWPPTHVRPRSVQDCA

/protein_id="AAD49615.1" /db_xref="GI:5733512"

/product="DR6"

codon_start=1

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AF015297
Human herpesvirus 6 (strain Uganda-1102).
Human herpesvirus 6 (strain Uganda-1102)
Viruses; daDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Roseolovirus.
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herpesvirus 6 (strain Uganda-1102) IE2hom mRNA,
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/gene="B4"
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/product="B4"
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/gene="B4"
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/rpt_unit=taaccc
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3250. .8711
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SNVTEFARRGLORDPVAYEEDLELPDRRMCGTNVRHLFDVIAAAADEHDLLTVGGLCQ
THAGVSCELLETVRDPWTAVPGVRMTLTVAAAQYRLMPDAAROLRLHLYAGHPLGPWI
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/db_xref="GI:5733516"
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CAAGCAAAGCCTCCAGCAGAGCCTCCAGCAGAGCCTCCAGCAGCAGGAGCCTCCAGCAGGGATT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soergel, A., Schiewe, U., Direct Submission
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  Similarity
                                                                                                                              1772
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                                                                                                                                                                                                      FEYKQIPKKPCNEKNLKEAVYDICCNGLSNNAAIIMYFTRSKKVAQIIKIMQKELMIR
PNITVSEAFKMNHAPPKYYDKDEIKRFIQLQKQGPQELWDKFENNTTHDLFSRHSDVK
                                                                                                                                                                                                                                                                                                          HNDQFYNPRFRPHIRTNRKKSESTNDTDSESSMSRCKSHCRNSPDSLTVVRRKKHKSG
SSSISSSIEENCRSNSHIVTGKEKFTPFYYQSSRTRSSSSSSSSSSASLSCSKSTLKTC
RKTQYKDNKQIKSKSDSKHKTTDMSSDYESNRHADVFKNSPEAGEKFPLHNSSPFNTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CKLKNPS IMDKNSAKNHTASADKNLTDNSP IRSNLNPTAFNKSNSNKS ITNST SNSDE
CTDRKPNCNSTKNDSKDPNRTCGKNSDKHLSKSCTMASKRAPSRASSRASSRDSSRAS
SRASSRASSRDSSRASSRBSSRDSSRASSRASSKASSRASSRASSRASSRASSRASSRDSSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRSDLKERKSNENEDKAVTKARDFSKLNPLLSPLPLTPEPAIDFADHTDKFYSTPEFN
QIQQNLHRSKTSLQDTVPISKHTPRAPTKDNSYKKHHDSKDNYPKMKHSPGRTTSKKN
TTNSNGHQNFKEVSVKNVSGKATSTSPKSKTHHYSSSSDEEGQYKSPVKTIIQSPSPY
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SNESGSTQVRFASELPNQLLQPMYTSHNQNANLQNNFTSLPYQPYRDPYRDIESSYRE
SRNTNRGYDYNFRHHPYRPRGGNGKYNYYNPNSKYQQPYKRCFTRTYNRRGRGHRSYD
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QSDNYNHFTKAQTIPETTKTKKHEATKDNETSTENQVLTPDVISLSYRPSSYKMDIIK
KIYDTDVIPLPKEALTANGSNRDVDIQKYKKAHIRCRSVQKKKERSSQTNKHDENHAS
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196. .4698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAB67722.1"
/db_xref="GI:2343283"
/translation="MEPAKPSGNNMGSNDERMQDYRPDPMMEESIKEILEESLMCDTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Human herpesvirus
/db_xref="taxon:10370"
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4.0%;
52.8%;
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92.2; DB 72
No. 6.4e-05;
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                                                                                                                                                                                                                                                                                                  polymerase; envelope protein; glycoprotein B; glycoprotein C; glycoprotein D; glycoprotein E; glycoprotein G; glycoprotein H; glycoprotein I; glycoprotein I; glycoprotein I; glycoprotein K; glycoprotein H; glycoprotein K; glycoprotein H; glycoprotein K; glycoprotein H; glycoprotein K; glycoprotein K; glycoprotein H; glycoprotein K; glycoprotein K; glycoprotein; minor capsid protein; membrane-associated phosphoprotein; minor capsid protein; neurovirulence factor; protease; protein; kinase; ribonucleotide reductase large subunit; ribonucleotide reductase small subunit; RL1 gene; UL2 gene; UR1 gene; UR2 gene; UR2 gene; UR3 gene; UR3 gene; UR3 gene; UR3 gene; UR4 gene; UR4 gene; UR4 gene; UR5 gene; UR
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McGeoch,D.J., Moss,H.W., McNab,D. and Frame,M.C.
DNA sequence and genetic content of the HindIII I region in the short unique component of the herpes simplex virus type 2 genome identification of the gene encoding glycoprotein G, and evolutionary comparisons
J. Gen. Virol. 68 (Pt 1), 19-38 (1987)
                                                                                                                                                      human herpesvirus 2.
human herpesvirus 2
viruses; dsDNA viruses, no RNA st
Alphaherpesvirinae; Simplexvirus.
1 (bases 1 to 154746)
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                                                                                                                                                                                                                                                                                          US3 gene; US4 gene; US5 gene; US6 gene; US9 gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    capsid associated tegument protein; capsid protein; compense; deoxyribonuclease; deoxyridine triphosphatase;
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13619
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complement(13338. .13341)
note="for RL1"
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complement(12685. .>13179)
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5124 c 4789 g 1893 t
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                                                                                                                                                                                                         no RNA stage; Herpesviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McGeoch, D.J., Cunningham, C., McIntyre, G. and Dolan, A. Comparative sequence analysis of the long repeat regions and adjoining parts of the long unique regions in the genomes of herpes simplex viruses types 1 and 2 J. Gen. Virol. 72 (Pt 12), 3057-3075 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (08-DEC-1999) A. Dolan, MRC Virology Unit, Churc
Street, Glasgow, G11 5JR, UK
On Dec 13, 1999 this sequence version replaced gi:1869820.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (25-FEB-1997) A. Dolan, Street,, Glasgow,, Gl1 5JR, UK revised bu [6]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Comparative DNA sequence analysis of the host shutoff genes of different strains of herpes simplex virus: type 2 strain HG52 encodes a truncated UL41 product encodes a truncated UL41 product 10.56n. Virol. 71 (Pt 6), 1387-1390 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dolan,A.
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/product="neurovirulence factor"
1738. .1743
2303. .5368
                                                                                                                                                                                                        /rpt_family="7"
461. .547
                                                                                                                                                                 /rpt_family="6"
943. .1070
                                                                                                                                                                                                                                                                                                     PEARARARARAHEDGGPAEEEEAAAAARGSSAAAGPGRRAV"
                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAB06759.1"
/db_xref="GI:1869821"
/db_xref="SWISS-PROT:P28283"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(440. .934,1089. .1379)
/gene="RL1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="RL1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1
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                                                                                                                                      rpt_family="5"
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join(2303.
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/db_xref="SWISS-PROT:P28284"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(4811)
                                        /codon_start=1
/product="uraci1-DNA glycosylase"
/protein_id="CAB06762.1"
/db_xref="GI:1869824"
                                                                                                                                                                                                   /translation="mgfyclfglyvmgawgawgggQateyylrsylakeygDllrwpc
mrtpaddvswryeapsyldyarldgiflryhcpgldtflwdrhagraylvnpflfaag
fledlshsyfpadtQetttrrallykeirdalgsrkQavshapyragcynedysrtrab
                                                                                                                                                                                                                                                             /product="virion glycoprotein L"
/protein_id="CAB06761.1"
/db_xref="GI:1869823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                issociated transcripts (LAT's)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="primary transcription initiation site for latency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="proposed LAT splice acceptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        function-"modulator of cell state and gene expression"
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db_xref="SWISS-PROT:P28275"
/translation="MFSASTTPEQPLGLSGDATPPLPTSVPLDWAAFRRAFLIDDAWR/
PLLEPELANPLTARLLAEYDRRCQTEEVLPPREDVFSWTRYCTPDDVRVVIIGQDPYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="proposed LAT splice donor site (5'AT species)"
                                                                                                                                      10211. .10978
/gene="UL2"
                                                                                                                                                                                                                                                                                                                         'gene="UL1"
                                                                                                                                                                                                                                                                                                                                                                                       note="start of UL (Long Unique region)"
                                                                                                        'gene="UL2"
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                                                                                                                         0211. .10978
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                                                                                                                      major capsid protein membrane-associated phosphoprotein; minor capsid protein; membrane-associated phosphoprotein; minor capsid protein; membrane-associated phosphoprotein; minor ribonucleotide reductase large subunit; ribonucleotide reductase small subunit; RI1 gene; RI2 gene; RS1 gene; tegument protein; thymidine kinase; UT15 gene; UT16 gene; UT11 gene; UT12 gene; UT18 gene; UT19 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAGGCGGAGGAGGAGGCGGCGGCGACCGCGGCCTG 122613
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capsid associated tegument protein; capsid protein; complete capsid associated tegument protein; capsid protein; complete genome; deoxyribonuclease; deoxyuridine triphosphatase; DNA polymerase; envelope protein; glycoprotein B; glycoprotein C; glycoprotein D; glycoprotein E; glycoprotein G; glycoprotein H; glycoprotein H; glycoprotein J; glycoprotein K; glycoprotein L; glycoprotein M; host shut-off factor; integral membrane protein; glycoprotein M; host shut-off factor; integral membrane protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Herpes simplex virus type 2 (strain HG52), complete genome.
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/translation="mymsrvysrsymsgvgeervpsaftilasmgwtfapqnhdpgas
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puttpiesiagtapdahyppldgepdrdaispltssvagdppgadgpyytfddilfwys
sidelgrqdlydiirdlrlslakfsiactktssfsgtaarqrkrgappqrtcvprsn
KSLQMFYLCKRANAAQVREQLRAVIRSRKPRKYYTRSSDGRLCPAVPVFVHEFVSSEP
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11019. .11024
11033. .11734
//gene="UL3"
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dsDNA viruses,
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LTVKRGAAASHSKLGWDRFVGGVVQKLAARRPGLVFMLWGAHAQNAIRPDPRQHYVLK
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/db_xref="GI:1869825"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA
    no RNA stage; Herpesviridae;
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Alphaherpesvirinae; Simplexvirus.

1 (bases 1 to 154746)

McGeoch, D. J., Woss, H.W., McNab, D. and Frame, M.C.

BNA sequence and genetic content of the HindIII 1 region

Short unique component of the herpes simplex virus type 2
identification of the gene encoding glycoprotein G, and
evolutionary comparisons

2 genome:

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Result
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Maximum Match 100%
Listing first 45 summaries
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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Appli

017753-025

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Query Match 4.2%;
Best Local Similarity 45.4%;
Matches 215; Conservative
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NAME/KEY:
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LOCATION:
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                                                                                                                CCCACGGTGTCACCTCGGCCCCGGACNNNAGGCCGNNNCCGGGCTCCACCGCCCCCNNNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region 457
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121..6166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region 439..5239
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58..120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Nucleotide 496
which is the codon for
or CCG; and Ala = GCT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Nucleotide 487 is Y = NNN
which is the codon for Thr or Asn wherein Thr =
or ACG; and Asn = AAT or AAC."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Nucleotide 457
which is the codon for
or CCG; and Ala = GCT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleotides and encodes The number of such repea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 101; DB 3
Pred. No. 2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 titute a repeated region who
nd encodes 20 amino acids, 1
such repeats varies from 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259;
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Pro or Ala wherein Pro
GCC, GCA, or GCG."
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Pro or Ala wherein Pro = GCC, GCA, or GCG."
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no acids, 17 of which are
les from 1 to 80."
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US-08-479-537A-4
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                                 FEATURE:
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                                                LOCATION:
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Sequence 4, Application US/08479537A Patent No. 5861381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (703) 836-202
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                       OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 08
FILING DATE: 04-APP-17-18
PRIOR APPLICATION NUMBER: US 08
FILING DATE: 04-APP-17-18
PRIOR NEET OF THE OBJECT O
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 01 FILING DATE: 14-MAR-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 07-JUN-1995
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MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
LOCATION:
                                                                                                                                                                                                 OTHER INFORMATION: OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                            NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States ZIP: 22313-1404
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Teskin, Robin L.
35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
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LATHE, Richard
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mat_peptide
121..5661
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58..120
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14-MAR-1995
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                                                                                                                  /note- "The nucleotides spanning
439-5239 constitute a repeated region wherein the repeat i
nucleotides and encodes 20 amino acids, 17 of which are fi
The number of such repeats varies from 1 to 80."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A MALIGNANT TUMOR
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Result
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Maximum Match 100%
Listing first 45 summaries
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
    seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Issued_Patents_NA:*
1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
7: /cgn2_6/ptodata/2,
                                                                                                                                                                                                                                                                                                                                                                         Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262060 seqs, 75620727 residues
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2348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/5C_COMB.seq:*
/cgn2_6/ptodata/2/ina/5D_COMB.seq:*
/cgn2_6/ptodata/2/ina/5C_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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    6192
6492
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               US-08-770-379-20

US-07-829-461A-8

US-08-781-891-209

US-08-676-967-5

US-08-676-974-5

US-09-08-487-5

US-09-098-487-5

US-08-781-891-208

US-08-946-026-32

US-08-452-531-208
                                                                                                                                                 US-08-479-537A-1
US-08-279-137A-4
US-08-232-463-14
US-09-130-114-2
US-09-130-114-2
US-09-130-114-1
US-09-130-114-1
US-07-884-811-15
US-07-884-811-15
US-07-885-971-15
US-08-194-088B-15
US-08-194-088B-15
US-08-194-088B-15
US-08-783-3-1
US-08-728-323A-1
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Sequence 1, Appli
Sequence 4, Appli
Sequence 14, Appli
Sequence 17, Appli
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Application 861381 CORMATION: CHAMBON, CHATHE, RIENY, M. INVENTION: HAREUTEN DENCE ADDRE PO. BOX Alexandria Virginia READABLE FO TYPE: Flow LICATION NOW POLICATION DA VICATION DA VICATION DA VICATION DA VICATION DA VICATION NOW POLICATION DA VICATION NOW POLICATION NOM POLICATION NOW POLICA	0000011000000000000000
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NMENTS COMPOSIT COMPOSIT REVENTION & MATHIS 0 00835 00835	52-531-1 60-746A-1 160-928B-3 110-928B-3 110-928B-3 110-928B-3 76-967-2 98-87-2 98-87-2 98-87-2 98-136-1 58-136-1 120-6351-78 58-136-2 120-6351-78 58-136-1 120-6351-78 58-136-1 120-6351-78 58-136-1 120-6351-78 58-136-1
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Best Local Similarity 45.4%;
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                       1885 ccatcggagaccccaggccccgcccggcaggacctgcaggggacgaaccagccgagagagc 1944
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NAME/KEY:
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NAME/KEY:
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OTHER INFORMATION:
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OTHER INFORMATION:
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CCCACGGTGTCACCTCGGCCCCGGACNNNAGGCCGNNNCCGGGCTCCACCGCCC
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58..120
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121..6166
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which is the codon for Thr or Asn wherein Thr =
or ACG; and Asn = AAT or AAC."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Nucleotide 457 is X1 = NNN
which is the codon for Pro or Ala wherein Pro =
or CCG; and Ala = GCT, GCC, GCA, or GCG."
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Pred. No. 1.3e-09;
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Sequence 4, Application US/08479537A Patent No. 5861381
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 514

PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMBER: FR 90/13101
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REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR91/00835
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 0: FILING DATE: 14-MAR-1995 ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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LOCATION: 457
OTHER INFORMATION:
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                                                                                                                    NAME/KEY: repeat_regrou
NAME/KEY: repeat_regrou
LOCARION: 439.5239
OTHER INFORMATION: /note= "The nucleotides spanning
OTHER INFORMATION: 439-5239 constitute a repeated region wherein the repeat i
OTHER INFORMATION: nucleotides and encodes 20 amino acids, 17 of which are fi
OTHER INFORMATION: The number of such repeats varies from 1 to 80."
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STREET: P.
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                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
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P.O. Box 1404
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LATHE, Richard
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SYSTEM: PC-DOS/MS-DOS
                                                         repeat_region
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     /note= "N
which is
or CCG; a
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     "Nucleotide 457 is X1 = NNN
is the codon for Pro or Ala wherein Pro = CCT,
; and Ala = GCT, GCC, GCA, or GCG."
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Best Local Similarity
Matches 25; Conserv
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APPLICANT: CHAMBO
APPLICANT: KIENY,
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CORRESPONDENCE ADDRESS: 5
CORRESPONDENCE ADDRESS: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                       APPLICATION NUMBER: FR 90/13101
FILING DATE: 23-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR91
FILING DATE: 23-OCT-1991
PRIOR APPLICATION DATA:
                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                          SOFTWARE: PatentIn Rel
                                                                                                                                                                      APPLICATION NUMBER: US/01
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                         CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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                             APPLICATION NUMBER: US 0 FILING DATE: 04-APR-1993
            FILING DATE: 04-APR-
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CATION NUMBER:
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KIENY, Marie-Paule
LATHE, Richard
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                                              US 08/039,320
                                                                                              WO PCT/FR91/00835
                                                                                                                                                                                                            US/08/479,537A
US 08/403,576
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LENGTH: 6192 base pairs
TYPPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity
Matches 161; Conserv
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LOCATION:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                               1585 ccatcggagaccccaggccccagcccagcaggacctgcaggggacgagccgagagc 1644
                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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                                                                                                                                                                                    LOCATION: 487
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                      NAME/KEY:
LOCATION:
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                                                                                   1765
                                                                                                                                                                                                                            461 CCCACGGTGTCACCTCGGCCCCGGACNNNAGGCCGNNNCCGGGCTCCACCGCCCCNNNG 520
                                                                                                               581
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OTHER INFORMATION:
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CCCACGGTGTCACCTCGGCCCCGGACNNNAGGCCGNNNCCGGGCTCCACCGCCCCNNNO-750
                                                                        CCCACGGTGTCACCTCGGCCCCGGACNNNAGGCCGNNNCCGGGCTCCACCGCCCCNN
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121..6166
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                                                                                                                                                                                                                                                                                                                                                                         /note= "Nucleotide 496 is x2 = NNN
which is the codon for Pro or Ala wherein
or CCG; and Ala = GCT, GCC, GCA, or GCG."
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Nucleotide 487 is y = NNN which is the codon for Thr or Asn wherein Thr or ACG; and Asn = AAT or AAC."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Nucleotide 457 is X1 = NNN
which is the codon for Pro or Ala wherein
or CCG; and Ala = GCT, GCC, GCA, or GCG."
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                                                                                                                                                                                                                                                                                                   Score 75.8;
Pred. No. 4.
                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                      8; DB 3;
4.6e-07;
                                                                                                                                                                                                                                                                                            193;
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1885

761 CCCACGGTGTCACCTCGGCCCCGGACNNNAGGCCGNNNCCGGGCTCCACCGCCC 814

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US-08-479-537A-4
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Patent No. 5861381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PILING DATE: 04-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (703) 836-202
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMBER: FR 90/13101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FR 90 FILING DATE: 23-OCT-1990 PRIOR APPLICATION DATA:
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TELEPHONE: (703) 836-6620
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STREE
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                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                    NAME/KEY: repeat_re LOCATION: 439..5239 OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION:
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 6449 base pairs
TYPE: nucleic acid
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P.O. Box 1404
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LATHE, Richard
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58..120
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                                                                                                        /note= "The nucleotides spanning 439-5239 constitute a repeated region wherein the repeat is unucleotides and encodes 20 amino acids, 17 of which are fixed the number of such repeats varies from 1 to 80."
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; LENGTH: 1931
; TYPE: DNA
; ORGANISM: EBNA
US-09-130-114-2
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Best Local Similarity
Matches 161; Conserv
                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                         sequence 2, Application US/09130114
Patent No. 5976807
                                                                                         SEQ ID NO 2
                                                                                                                            APPLICANT: Robbins, Alan K.

TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
TITLE OF INVENTION: From Multiple Transfected Episomes
FILE REFERENCE: 0867/11903US1
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
                                                                                                                                                                                                                APPLICANT: Horlick, Robert A. APPLICANT: Damaj, Bassam B.
                                                                                                    SOFTWARE:
                                                                                                                   NUMBER OF SEQ
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NAME/KEY:
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milarity 45.5%;
Conservative
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                                                                                                       for Windows Version 3.0
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which is the codon for Pro or Ala wherein Pro or CCG; and Ala = GCT, GCC, GCA, or GCG."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Nucleotide 496 is x2 = NNN
which is the codon for Pro or Ala wherein
or CCG; and Ala = GCT, GCC, GCA, or GCG."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Nucleotide 487 is y = NNN which is the codon for Thr or Asn wherein Thr = ACT, ACC, or ACG; and Asn = AAT or AAC."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 75.8;
Pred. No. 4.
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Length 1931;
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Query Match Best Local Similarity

63.8%;

Score 74.6; DB 4; Pred. No. 6.4e-07; THIS PAGE BLANK (uspto)

Run on:

Sequence

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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                     75.88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Issued_Patents_NA:*

1: /ggn2_6/ptodata/2,

2: /cgn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

4: /cgn2_6/ptodata/2,

5: /cgn2_6/ptodata/2,

6: /ggn2_6/ptodata/2,

7: /cgn2_6/ptodata/2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match
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2290
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Gapop 10.0 , Gapext 1.0
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/5C_COMB.seq:*
/cgn2_6/ptodata/2/ina/5C_COMB.seq:*
/cgn2_6/ptodata/2/ina/5C_COMB.seq:*
/cgn2_6/ptodata/2/ina/FCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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     US-08-232-463-14
US-08-479-537A-1
US-08-479-537A-1
US-08-479-537A-4
US-09-130-114-2
US-09-130-114-2
US-09-130-114-1
US-07-884-811-15
US-07-885-971-15
US-08-194-088B-15
US-08-194-087-15
US-08-194-087-15
US-08-719-379-17
US-08-770-379-17
US-08-770-379-17
US-08-781-891-209
US-08-781-891-209
US-08-781-891-208
US-08-676-967-5
US-08-676-967-5
US-08-676-974-5
US-08-676-746-026-32
US-08-460-7468-2
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Sequence 14, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 15, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 1, Appli Sequence 1, Appli Sequence 20, Appli Sequence 20, Appli Sequence 5, Appli Sequence 20, Appli Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                               ; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
US-08-232-463-14
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US-08-232-463-14/c
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                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMPLECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAX: (703)883-4109
                                                                                                                                                                                                       TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILLING DATE:
CONTROL OF THE PROPERTY O
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 5
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKMER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                             LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CITY: Alexandria
STATE: VA
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ZIP: 22313-0299
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1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-452-531-1
US-08-460-746A-1
US-08-676-967-2
US-08-676-974-2
US-09-98-487-2
US-09-98-487-2
US-08-36-6511-23
PCT-08-58-136-2
US-08-658-136-1
US-08-658-136-1
US-08-658-136-1
US-08-658-136-1
US-08-658-136-1
US-08-658-136-1
US-08-466-6031-1
US-08-466-6031-1
US-08-466-717-1
US-08-466-717-1
US-08-466-713-1
US-08-466-713-1
US-08-466-713-1
US-08-363-413-22
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                                                           STREET: P.O. BOX 1404

CITY: Alexandria

STATE: Virginia
COUNTRY: United States
COUNTRY: United States
ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CORRENT APPLICATION NUMBER: US/08/479,537A
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: FR 90/13101
FILING DATE: 23-CCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WS 0/13101
FILING DATE: 23-CCT-1991
PRIOR APPLICATION NUMBER: WS 0/13101
FILING DATE: 23-CCT-1991
PRIOR APPLICATION NUMBER: WS 0/13101
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Best Local Similarity 6.08
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: CHAMBO
APPLICANT: KIENY,
                      FILING DATE: 04-APR-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1302 cctcaggacggggacccaggaagtgggcggtcaggaccctgggggaggcagtgcagccctg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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P.O. Box 1404
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LATHE, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAREUVENI, Mara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAMBON, Pierre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TREATMENT: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHARMACEUTICAL COMPOSITION FOR THE TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
                                                                                                                                     WO PCT/FR91/00835
Sn
08/403,576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWECKER & MATHIS, L.L.P
                                                                                                                                                                                                                                                                                                                                                     Version
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Best Local Similarity 45.:
Matches 161; Conservative
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6192 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
FEATURE:
NAME/KEY:
                         1705
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LOCATION: 439..5239
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                581
                                                                                                                                                                                                                                                     461 CCCACGGTGTCACCTCGGCCCCGGACNNNAGGCCGNNNCCGGGCTCCACCGCCCCNNNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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OTHER INFORMATION:
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: /note= "Nucleotide 457 is X1 = NNN
OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro =
OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Teskin, Robin L. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
CCCACGGTGTCACCTCGGCCCCGGACNNNAGGCCGNNNCCGGGGCTCCACCGCCCCCNNNG
                                                                                      CCCACGGTGTCACCTCGGCCCCGGACNNNAGGCCGNNNCCGGGGCTCCACCGCCCCCNNNG 580
                                                                                                                           CCCACGGTGTCACCTCGGCCCCGGACNNNAGGCCGNNNCCGGGCTCCACCGCCCCCNNNG
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121..6166
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58..120
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                                                                                                                                                                                                                                                                                                                                     3.3%;
45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Nucleotide 496
which is the codon for
or CCG; and Ala = GCT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Nucleotide 487 is Y = NNN which is the codon for Thr or Asn wherein or ACG; and Asn = AAT or AAC."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "The nucleotides spanning
439-5239 constitute a repeated region wherein the repeat
nucleotides and encodes 20 amino acids, 17 of which are
The number of such repeats varies from 1 to 80."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35,030
                                                                                                                                                                                                                                                                                                                    Score 75.8; DB 3;
Pred. No. 4.1e-07;
0; Mismatches 193;
                                                                                                                                                                                                                                                                                                                      193;
                                                                                                                                                                                                                                                                                                                                                                                                           is X2 = NNN
Pro or Ala wherein Pro = CCT,
GCC, GCA, or GCG."
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US-08-479-537A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: CHAMBON, Pierre
APPLICANT: KIENY, Marie-Paule
APPLICANT: LATHE, Richard
APPLICANT: HAREUVENI, Mara
                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703) 836-2021 NFORMATION FOR SEQ ID NO:
                                                                                                                                                          NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLIANCE: 23-OCT-127.
FILING DATE: 23-OCT-127.
PRIOR APPLICATION NUMBER: WO PCT/FR91/00835
APPLICATION NUMBER: 23-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 04-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,576
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,537A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: HAREUVENI, MATA
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 90/13101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                  OTHER INFORMATION:
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NAME/KEY:
LOCATION:
                                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                     LENGTH:
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                                                                                                                                                                                                                                                                                 nucleic acid
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Teskin, Robin L.
35,030
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P.O. Box 1404
 mat_peptide
121..5661
                                                                                                                        repeat_region 439..5239
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58..120
                                                                                                                                                                                                                                 DNA (genomic)
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                                                  /note= "The nucleotides spanning 439-5239 constitute a repeated region wherein the repeat nucleotides and encodes 20 amino acids, 17 of which are f The number of such repeats varies from 1 to 80."
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SOFTMARE: FASTSE
SOFTMARE: FASTSE
SEQ ID NO 2
LENGTH: 1931
TYPE: DNA
ORGANISM: EBNA
US-09-130-114-2
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; Sequence 2, Application US/09130114

; Patent No. 5976807
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Best Local S
Matches 161
                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Horlick, Robert A.
APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing
TITLE OF INVENTION: From Multiple Transfected Episomes
FILE REFERENCE: 0867/1D903US1
                                                                                                             CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
                                                                                                NUMBER OF SEQ ID NOS:
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LOCATION: 457
OTHER INFORMATION:
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LOCATION:
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Local Similarity 45.5%;
nes 161; Conservative
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OTHER INFORMATION:
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                                                                                 FastSEQ
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                                                                                 for Windows Version 3.0
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which is the codon for Pro or Ala wherein
or CCG; and Ala = GCT, GCC, GCA, or GCG."
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which is
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which is the codon for Pro or Ala wherein
or CCG; and Ala = GCT, GCC, GCA, or GCG."
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Query Match Best Local Similarity

63.8%;

Score 74.6; DB 4; Pred. No. 5.7e-07;

Length

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US-09-050-863-2
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                                                                                                                                        Query Match
Best Local S
Matches 229
                                                                                                                                                                                                                                                                                       NAME: S11va, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-65
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEPAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application Patent No. 6114111 GENERAL INFORMATION:
APPLICANT: Lao, Ying
                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
1073 cacggagcgtggagccccaggatgcgggacccctggagaggagccagggggatgaggcag
                                                                1016
                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 2580 base pairs
                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hiang, Bétty
APPLICANT: Payan, Don
TITLE OF INVENTION: Mammalian Protein Interaction Cloning
TITLE OF INVENTION: System
NUMBER OF SEQUENCES: 5
COMPRESSION SECURITIES: 5
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                                                                                                   956 ggaaggtggaggaaggaagccccggggaaccccgaccacgaggccagcacccagggtc 1015
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                                                                                                                                       Match 2.9%; Local Similarity 47.7%; Local Similarity 47.7%; les 229; Conservative
                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: unkno
                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 3 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                                        ggacctgtgggccagaggcatagcaagggtgg---gggcagggtggacgagggggccccagc 1072
                                                                                  gcggccgctgaattctagccgagcatggaccccgactgcgactccacctgggaggag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGGACGAGGACGGGGAGGACGGGGAGGACGGGGAGGACGAGGACGAGGAC 884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA
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4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                    Score 67.2; DB 5;
Pred. No. 1.9e-05;
0; Mismatches 248;
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                                                                                                                                       248;
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                                                                                                                                                              Length 2580;
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APPLICANT: Horlick, Robert A.

APPLICANT: Damaj, Bassam B.

APPLICANT: Damaj, Bassam B.

APPLICANT: Robbins, Alan K.

ITILE OF INVENTION: Eukaryotic Cells Stably Expressing Gen

ITILE OF INVENTION: From Multiple Transfected Episomes

FILE REFERENCE: 0867/1D903US1

CURRENT APPLICATION NUMBER: US/09/130,114

CURRENT FILING DATE: 1998-08-06

NUMBER OF SEQ ID NOS: 36

SOFTWARE: FastSEQ for Windows Version 3.0

IENGTH: 5452

TYPE: DNA

ORGANISM: VEBNA

US-09-130-114-1
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US-09-130-114-1/c
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Best Local Similarity
Matches 229; Conserv
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Pred. No. 2.2e-05;
0; Mismatches 248;
                                                                                                                                                                                                                                                                                                                                                                                                    248;
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US-07-884-811-15
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TELEX: 910/371-7168
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
TENGTH: 10596 bases
                                                                                                                                                                                                                                         2.9%;
Best Local Similarity 47.7%;
Matches 229; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15, Application US/07884811 Patent No. 5316921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/
FILING DATE: 19920518
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                          1016
                                                                                                                            2347
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Genentech,
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REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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ggggccacggggaagataggccggagcccttaagccccaaagagagcaagaagaggaagc 1192
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EDNESS: single
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    Paul J. Lokker, Nathalie A. Mark, Melanie R.
SINGLE-CHAIN HEPATOCYTE GROWTH FACTOR VARIANTS

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Pred. No. 2.5e-05;
0; Mismatches 248;
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US-07-885-971-15
                                                                                                                                                                                                US-07-885-971-15
                                                                                                                    Query Match 2.9%;
Best Local Similarity 47.7%;
Matches 229; Conservative
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APPLICANT: Godows
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/
FILING DATE: 19920518
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                   1016 ggacctgtgggccagaggcatagcaagggtgg---gggcagggtggacgagggggccccagc 1072
                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-3216
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SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                        TELEPHONE: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                 NAME: Dreger, Ginger R. REGISTRATION NUMBER: 33 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                             STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                           LENGTH: 10596 bases
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tgggagccagggtggccgacaaggtgaggaagcggaggaaggtggatgagggtgctgggg
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HEPATOCYTE GROWTH FACTOR PROTEASE DOMAIN VARIANTS
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                                                                                                                  Score 67.2; DB 1;
Pred. No. 2.5e-05;
0; Mismatches 248;
                                                                                                                     248;
                                                                                                                                                Length 10596;
                                                                                                                     Indels
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Pred. No. 2.5e-05;

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US-08-087-783A-15

: Sequence 15, Application US/08087783A

: Patent No. 5547856
US-08-087-783A-15
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy di
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,783A
FILING DATE: 13-Jul-1993
CLASSIFICATION: 435
                                                                         TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                 APPLICATION NUMBER: 07/885971 FILING DATE: 18-MAY-92 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 07, FILING DATE: 18-MAY-92 PRIOR APPLICATION DATA:
                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: GODOWSKI, Paul J., LOKKEY, TITLE OF INVENTION: HEPATOCYTE GROWTH NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1313
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                                                                                                                                                                               NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0755779P1
                             TYPE: Nucleion STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 460 Point San Bru
CITY: South San Francisco
                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                             H: 10596 base pairs
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               Linear
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                            Single
                                                                                                                                                                                                                                                                                                                   07/884811
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Query Match

2.9%;

Score 67 <u>.</u>2

В 1;

Length

10596;

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RESULT 10
US-08-194-088B-15
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                                                                                                                                             APPLICATE: 09-FEB-1>>>
FILING DATE: 09-FEB-1>>>
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/884
APPLICATION DATE: 18-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 47.7
Matches 229; Conservative
               TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                          FILING DATE: 18-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gallegos, R. Thomas
REGISTRATION NUMBER: 32,692
REFERENCE/DOCKET NUMBER: 7551
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415,225-2614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc
STREET: 460 Point San Bru
CITY: South San Francisco
STATE: California
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2527
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                              TELEPHONE: 415/2-1981
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.r: 10596 bases
rypE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-194-088B-15
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US-08-194-087-15
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GENERAL INFORMATION:
APPLICANT: Godowski, Paul J. Lo
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Best L
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MEDIUM TYPE: 5.25 inch, 360 Kb i
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1016
                                                 APPLICATION NUMBER: US/0:
FILING DATE: 18-MAY-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         2407
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                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                      STREET: 460 Point San Bruno Blvd CITY: South San Francisco
STATE: California
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                                      APPLICATION NUMBER:
                                                                                                                                                                                             COUNTRY:
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HEPATOCYTE GROWTH FACTOR PROTEASE DOMAIN VARIANTS
                                                                                        us/08/194,087
                                                                                                                                                     360 Kb floppy disk
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Pred. No. 2.5e-05;
0; Mismatches 248;
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RESULT 12
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 10596 bases
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                        Sequence 15, Application PC/TUS9304648 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.9%;
Best Local Similarity 47.7%;
Matches 229; Conservative
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb fl
COMPUTER: IBM PC compattible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/0464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 779
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEPAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                    1373
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                                                                                                                                                                                                             APPLICANT: Genentech, Inc., God
TITLE OF INVENTION: HEPATOCYTE
NUMBER OF SEQUENCES: 21
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ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                                                       2587
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                                                                                                                                     STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gyacctgtgggccagagcatagcaagggtgg---gggcaggggtggacgagggggccccagc 1072
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                                                                            360 Kb floppy
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Pred. No. 2.5e-05;
                                                                                                                                                                    Blvd
                                                                                                                                                                                                                               Paul J., Lokker, FACTOR VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3;
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Sequence 17, Application US/08770379
Patent No. 5849564
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: RUSSO, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: MOOIE, PATRICK S.
TITLE OF INVENTION: POLYPEPTIDES F.
                                                                                                                                 RESULT 13
US-08-770-379-17
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Best Local Similarity 47.7%;
Matches 229; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 19930517
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 07/8
FILING DATE: 18-MAY-92
PRIOR APPLICATION NUMBER: 07/8
                                                                                                                                                                                          2347
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REGISTION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 75;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 10596 bases
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ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                 tgggagccagggtggccgacaaggtgaggaagcggaggaaggtggatgagggtgctgggg 1432
                                                                                                                                                                                                                                                   ggacccaggaagtgggcggtcaggaccctggggaggcagtgcagccctgccgccaacccc 1372
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Pred. No. 2.5e-05;
0; Mismatches 248;
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   KAPOSI'S
   SARCOMA-ASSOCIATED
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Best Local Sim
Matches 195;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 5234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
 24637
                                                     24581 CCCCAGGAGCCCCGGCAGCACCCCAGGAGCCCCGGCGCGCCA----
                                                                                                                                                                                                                    24461
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MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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ADDRESSEE: Cooper & Dunham
STREET: 1185 Avenue of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 35100 base pairs TYPE: nucleic acid STRANGENESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE:
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STATE: New York
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GGATCCCGGCGCGCCCCCCCCCGGAGGGGGA 24669
                                                                     CCCCAGGAGCCCCGGCAGCACCCCAGGAGCCCCCAGGAGCCCCCAGGAGCCCCAGGAGCA
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Pred. No. 6.2e-05;
1; Mismatches 193;
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RESULT 14 US-07-945-283-1 ; Sequence 1, Application ; Patent No. 5352596

US/07945283

GENERAL INFORMATION:

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US-07-945-283-1
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Best Local Similarity
Matches 87; Conserv
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APPLICATION NUMBER: US/07/
FILING DATE: 19920911
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Ribando, Curtis P
REGISTRATION NUMBER: 27976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 309-685-4128 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY:
                                                                                                5596
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ADDRESSEE: Curtis P. Ribando
STREET: 1815 No. 5352396th University Street
                                          5656
                                                                                                                                                                                                                                                                 LOCATION: FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 309-685-4011 ext.513
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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LENGTH: 8438 base pairs
              183
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LOCATION:
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ggcgcggcc 191
                                         GGCGGCGGCGGCGGGGGGCCCGGGGGGCGGAGGCGGGCCGGGGAGAGGTCCGA 5715
                                                          cyccygcycyaygyacycygacyayygacyayyaytcygyaycogcycygyc 182
                                                                                             ggaggaggacgaggatgcggaggacgcggggggacgaggactgcgaggacggcgaggc 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 double
                                                                                                                                                                 2.7%;
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Involving The EPO and LLT Genes
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Pred. No. 0.0003;
                                                                                                                                                      Mismatches
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US-08-728-323A-1
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                                                                                                                                                                                                                                                                     Query Match 2.0
Best Local Similarity 57.0
Matches 107; Conservative
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APPLICANT: Chang, Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 212-278-040
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: Immediate Early Protein From Kaposi's
TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA
TITLE OF INVENTION: Encoding Same And Uses Thereof
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/728,323A FILING DATE:
                                                                 1148
                                                                                                                                   1088 AGGATGACGAGGATGACGAGGAGGATGACGAGGATGACGAGGAGGATGACGAGG 1147
                                                                                                                                                                                                   1028 AGGATGACGAGGAGGATGACGAGGAGGATGACGAGGATGACGAGGATGACGAGG 1087
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1208 AGGAG 1212
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                               182 cggcg 186
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                                                                                                                                                                   62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
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ZIP: 10036
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                                                                 agaattcagcggccgctgaattctagccgagcatggacgaccccgactgcgactccacct 61
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E: New York
TRY: U.S.A.
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1185 Avenue of the Americas
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Russo, James J.
                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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Pred. No. 0.00053;
0; Mismatches 78;
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Search completed: October 12, 2000, 17:09:44 Job time: 28148 sec

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Result
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Maximum
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Maximum Match 100%
Listing first 45 s
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Perfect score:
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     seq
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length: 2000000000
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5E_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/5C_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/5C_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/6_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
7: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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Gapop 10.0 , Gapext 1.
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1232
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5.0
4.7
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Copyright (c) 1993 - 2000 Comp
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      Length
    BB
  US-09-130-114-2
US-07-945-283-1
US-08-781-891-209
US-08-781-891-209
US-08-78-323A-1
US-08-676-967-5
US-08-676-974-5
US-08-676-974-5
US-08-98-487-5
US-08-98-487-2
US-08-98-658-136-1
US-08-658-136-1
US-08-658-136-2
US-08-658-136-1
US-08-658-136-1
US-08-676-974-2
US-08-676-974-2
US-08-676-974-2
US-09-098-487-2
US-09-098-487-2
US-09-130-114-1
US-07-885-971-15
US-08-087-783A-15
US-08-087-783A-15
US-08-194-088B-15
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Sequence 2, Appli
Sequence 1, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 20, Appli
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Sequence 6, Appli
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Sequence 8, Appli
Sequence 7, Appli
Sequence 2, Appli
Sequence 15, Appli
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                                              RESULT 2
US-07-945-283-1
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US-09-130-114-2/c
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Best Local Similarity
Matches 124; Conserv
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US-08-650-766-2	US-08-967-727-5	US-08-142-368A-5	US-08-299-849B-5	US-07-807-043B-5	US-08-967-727-4	US-08-142-368A-4	US-08-299-849B-4	US-07-807-043B-4	US-08-967-727-2	US-08-142-368A-2	US-08-299-849B-2	US-07-807-043B-2	US-08-263-413-22	US-08-263-413-23	US-08-785-420-1	US-08-458-568A-11	US-08-690-473-1	PCT-US93-04648-15
e 2	•	Sequence 5,	Sequence 5,	Sequence 5,	Sequence 4,	Sequence 4,	Sequence 4,	Sequence 4,	Sequence 2,	Sequence 2,	Sequence 2,	Sequence 2,	Sequence 22,	Sequence 23,	Sequence 1,	Sequence 11,	Sequence 1,	Sequence 15,
Appl	Appli	App1:	Appl	Appl	Appl	Appl	Appl	Appl	Appl	App1	App1	Appl	`	•	Appl	, App	Appli	, App

ALIGNMENTS

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; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: EBNA
US-09-130-114-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: HOrlick, Robert A.
APPLICANT: Damaj, Bassam B.
APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
APPLICANT: Robbins, Alan K.
APPLICANT: ROBBINS, Alan K.
TITLE OF INVENTION: From Multiple Transfected Episomes
FILE REFERENCE: 0867/10903US1
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08
Sequence 1, Application Patent No. 5352596 GENERAL INFORMATION: APPLICANT: Cheung, A
                                                                                                                                                                                                                                                                                                                      ggcgcggcccagctcgttccagtccagaatgacagggtccagaaactggcgagccacgag
                                                                                                                                                                                                                                                                                                                                            gccggcgagggacgcggacgcaggggacgaggacgagga-gtcggaggagccgcggggc 183
                                                                                                                                                                                                                                                                                                                                                                                                                         gaggaggacgaggatgcggaggacgcggaggacgaggactgcgaggacggcgaggcc 124
                                                                                                                                                                                                                                           Conservative
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  Andrew K.
                                                           US/07945283
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Pred. No. 3.2e-07;
0; Mismatches 68;
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; LOCATION:
US-07-945-283-1
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Best Local (
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TELEFAX: 309-685-4128
INFORMATION FOR SEQ ID NO: 1:
 5716
                                                   5656
                                                                                                    5596
                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0: FILING DATE: 19920911 CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                       FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 8438 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 309-685-4011 ext.513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis P. Ribando
STREET: 1815 No. 5352596th University Street
                         184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: I
                                                                           124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wesley, Ronald D.
TITLE OF INVENTION: Pseudora.
TITLE OF INVENTION: Involvin.
NUMBER OF SEQUENCES: 7
                                                                                                             64 ggaggaggacgaggaggatgcggaggacgcggaggacggaggactgcgaggacggcgaggc 123
                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
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LOCATION:
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                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ribando, Curtis P
REGISTRATION NUMBER: 27976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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GTCGCTGCC 5724
                       ggcgcggcc 192
                                              87;
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                                                                                                                                                      Conservative
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replace(1267, "t")
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622..6495
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                                                                                                                                                               5.0%; Score 61.8; DB 1; 67.4%; Pred. No. 7.1e-05;
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                                                                                                                                                    Mismatches
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                                                                                                                                                    42;
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RESULT 4
US-08-728-323A-1
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; TOPOLOGY: linear
US-08-781-891-209
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US-08-781-891-209/c
Sequence 1, Application US/08728323A Patent No. 5948676
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
                                                                                                                                                                                                                                                                                                                                                               Query Match 4.7%;
Best Local Similarity 66.9%;
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (206) 682-60
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 51259 base pai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/781,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
                                                                                                                                                                  131 GGAG 128
                                                                                                                                                                                               184
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                                                                                                                                                                                                                                                                                                                64 ggaggaggacgaggatgcggaggacgcgaggacgaggactgcgaggacggcgaggc 123
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FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: No. 6090620tenburg Ph.D., Carol REGISTRATION NUMBER: 39,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE:
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5. 6090620
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Yu, Chang-En
Oshima, Junko
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00 Columbia Center,
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682-6031
MO: 209:
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Pred. No. 0.00054;
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                                                                                                                                                                                                                                                                                                                                                                                          Length 51259;
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APPLICANT:

Edelman, Isidore S.

APPLICANT: MOORE, PAITILE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:

Encoding Same And Uses Thereof

Immediate Early Protein From Kaposi's Sarcoma-Associated Herpesvirus, DNA

Patrick S.

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Best Local s
                                                                                                                                                          Sequence 14, Application US/08232463 Patent No. 5670367
                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEPAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                     1077
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
          CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road,
                                                                                                                                                                                                                                                           1197
                                                                                                                                                                                                                                                                                                                       1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, V. CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/728,323A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UZIP: 10036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                       GGAG 1200
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Alexandria
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1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U.S.A.
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               Suite 500
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RESULT 6
US-08-770-379-20/c
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILING DATE: 26-AUG-1991
ANTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                       APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT: Edelman, Isidore S.
APPLICANT: MOOTE, PATITICK S.
TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THERE
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1339
                                                                                                                                                                                                                                                                                     1159
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                           1099 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRATCGCAAGCTCCC 1054
                                                                                                                                                                                                                                                                                                                                                                             183
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                                                                                                                                                                                                                                                      303 acacgccaaacctgagtttctacagaaatgagatccgcttcctgcc 348
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: EP 9 FILING DATE: 26-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  gggacatgtgtaggtatcggcacaactatccggatctggtggaacgagactgcaatgggg
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                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 2.4%; Pro 7; Conservative 181;
                                                                                                                                                  Application US/08770379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7218 base pairs
                                                                         Bohenzky, Roy A.
Russo, James J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (703)683-4109
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Pred. No. 0.00081;
31; Mismatches 98;
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CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFIERENCE/DOCKET NUMBER: 5234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08676967 Patent No. 5747317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 4.6%;
Best Local Similarity 66.1%;
Matches 82; Conservative
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                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                              MEDIUM TYPE: Floppy
                                                                                                                                                                                              NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSE: Science & Technology Law Group
STREET: 268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                              TITLE OF INVENTION: Human Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                             184 ggcg 187
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FILING
               APPLICATION NUMBER:
                                                                                                                                  ZIP: 94104
                                                                                                                                            COUNTRY:
                                                                                                                                                                                CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: 11
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                 us/08/676,967
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Pred. No. 0.0011;
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US-08-676-974-5
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Patent No. 5770422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 4.5%;
Best Local Similarity 55.1%;
Matches 151; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: OSMAN Ph.D., Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCB96-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEPHONE: (415)343-4342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415)343-434
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                        ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Datentin Release #1.0
           ATTORNEY/AGENT INFORMATION:
NAME: OSMAN Ph.D., Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCBS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                 APPLICANT: COLLINS, KATHLEEN
TITLE OF INVENTION: Human Telomerase
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Science & Technology Law Group
STREET: 268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                    STREET: 200 LL.
CITY: San Francisco
STATE: CA
                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
TYPE: nucleic acid
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                                                                                                                                        APPLICATION NUMBER:
                                                                                                      CLASSIFICATION:
                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                     COUNTRY: UZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 ggaggaggacgaggatgcggaggacgcgggaggacgaggactgcgaggacggcggaggc 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGCAGCGACCACAGCGAGGAGGACCAGCGACGGAGGAGCGACAGCATCGACGACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAAGGTGACCAAGCCCGTGCAGATCCAGAAGCGCCCGTGAAGCGCCCCGCCCAA 836
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                                                                                                                                                                      PatentIn Release #1.0, Version
(415)343-4341
                                                                                                                                          us/08/676,974
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                                 UCB96-055
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Pred. No. 0.00095;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120;
                                                                                                                                                                            #1.30
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TELEFAX: (415)343-434 INFORMATION FOR SEQ ID NO:

(415)343-4342

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RESULT 9
US-09-098-487-5
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       REFERENCE/DOCKET NUMBER: UCB9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEPAX: (415)343-4342
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09098487 Patent No. 5917025
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Best Local Similarity 55.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION: APPLICANT: COLLIN
                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/098,487
                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: COLLINS, Kathleen TITLE OF INVENTION: Human Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: UZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Science & Technology Law Group STREET: 268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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Pred. No. 0.00095;
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RESULT 10
US-08-781-891-208/c
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US-08-781-891-208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
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Best Local
                                                                                                                                                                                 SOFTWARE: Patentin Release #10, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6090620tenburg Ph.D., Carol REGISTRATION NUMBER: 39,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 151;
                                         TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 208:
SEQUENCE CHARACTERISTICS:
LENGTH: 16442 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                        CLL.
STATE: W.L
COUNTRY: USA
TO: 98104-7092
TD: TDADABLE FY
                                                                                                                                    REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED
TITLE OF INVENTION: WERNER'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               837
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COMPUTER: IBM PC
OPERATING SYSTEM:
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                              STRANDEDNESS:
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5. 6090620
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Similarity 55.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington
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Yu, Chang-En
Oshima, Junko
Mulligan, John T
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                linear
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Pred. No. 0.00095;
0; Mismatches 120; Indels
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US-08-946-026-32
                                                                                                                                                                                                                            US-08-946-026-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. DURANTION:
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Dillon, Davin C.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Mitcham, Jennifer L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND IMMUNODIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: AND IMMUNODIAGNOSIS OF PROSTATE CANCER
                                                                                                                                       Query Match
Best Local S
Matches 80
                                                                                                                                                                                                                                                       TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 768 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 83; Conserv
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NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 2101

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-6900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,026
FILING DATE: 07-OCT-1997
CLASSIFICATION: 424
CLASSIFICATION: 424
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MEDIUM TYPE: Floppy disk
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                   129 gcgcgagggacgcgggacgcggggacgaggacgaggagtcggaggagccgcggggcgc 188
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CITY: Seattle
STATE: Washington
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 69 aggacgaggaggatgcggaggacgcggaggacggaggacggcggcggcgcgcg 128
                                                                                                                               4.4%;
Local Similarity 65.6%;
es 80; Conservation
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ZIP: 98104-7092
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ilarity 64.8%;
Conservative
                                                                                                                                                                                                                                            linear
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                                                                                                                                       Score 54.8; DB 5; Length 768; Pred. No. 0.0014; O; Mismatches 42; Indels
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US-07-829-461A-8
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GENERAL INFORMATION:
                                                                                                                                                                                         Matches
                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                         PILING DATE: January 31, 1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/739,05
PRIOR APPLICATION UMBER: 07/561,96
APPLICATION UMBER: 07/561,96
APPLICATION DATA:
APPLICATION UMBER: 07/561,96
APPLICATION UMBER: 07/561,96
APPLICATION UMBER: 03/251
APPLICATION UMBER: 03/251
APPLICATION UMBER: 03/251
                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (303) 850-94 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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TITLE OF INVENTION: Systematic Polypeptide
TITLE OF INVENTION: Evolution by Reverse
TITLE OF INVENTION: Trnslation
                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 850-9900
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                100 cgaggactgcgaggacggcgaggccgccgggggaggacgcggggacgcaggggacgagga 159
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122
                           160 cgaggagtcggaggagccgcggg 182
                                                                62
                                                                                                                                                                                                                                                                                               LENGTH: 150 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM con
OPERATING SYSTEM:
                                                                                                                                             40 gaccccgactgncgactccacctgggaggaggacgaggaggatgcgggaggacgcgggagga 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 4582
CITY: Denver
                                                                                                                                                                                                     Match 4.3%;
Local Similarity 60.1%;
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CGACGACGCCATGGTTGCGATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Beaton & Swanson, P.C. 4582 South Ulster Street Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                       linear
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January 31, 1992
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                                                                                                                                                                                                                                                                                                                                                             3) 650

) 850-9401

3 NO: 8:
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                                                                                                                                                                                    Score 52.4; DB 3; ... Pred. No. 0.0033; ... wiematches 57;
144
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                                                                                                                                                                                                                       Length 150;
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RESULT 13 US-08-306-691B-23

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RESULT 14
PCT-US93-06251-78
PCT-US93-06251-78
; Sequence 78, Application PC/TUS9306251
; GENERAL INFORMATION: Eric and Rife, Jason P.
; APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonat
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best
                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US FILING DATE: September CLASSIFICATION: 514
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Diskette, 3.50 inch, 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Calabretta, Bru
APPLICANT: Skorski, Tomasz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: ANTISENSE TARGETING COOPERATING ONCOGENES NUMBER OF SEQUENCES: 55
                                                                                                                                                                                                                                                                                                             160 GGAGGG 165
                                                                                                                                                                                                                                                                               184
                                                                                                                                                                                                                                                                                                                             40
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OPERATING SYSTEM: 1
SOFTWARE: WordPerf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Monaco, Daniel A. REGISTRATION NUMBER: 30,480
                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 79; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                            ggcgcg 189
                                                                                                                                                                                                                                                                                                                                                                          SSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
T: Two Penn Center, Suite 1800
Philadelphia
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DN: 514
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62.7%;
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Pred. No. 0.
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0.012;
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RESULT 15
US-08-658-136-2/c
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; MOLECULE TYPE:
PCT-US93-06251-78
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Patent No. 607171
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APPLICANT: KLINGE
APPLICANT: LANDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
                                           MEDIUM TYPE: Floppy
                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
                                                                                                                                                                                        TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE NUMBER OF SEQUENCES: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 2301 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                        APPLICANT: GERMINO, GIAPPLICANT: QIAN, FENG
                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 GGAGGG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 ggcgcg 189
                                                                                                                           ADDRESSEE: GENZIBLE CORRECT: ONE MOUNTAIN ROAD
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 ggaggaggacgaggatgcggaggacgcggaggacgaggactgcgaggacggcgaggc 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity nes 79; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                             MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                    Application US/08658136
                                                                                                                                                                                                                                     LANDES, GREGORY M
BURN, TIMOTHY C
CONNORS, TIMOTHY D
DACKOWSKI, WILLIAM
GERMINO, GREGORY
                                                                                              USA
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                                                                                                                                                                                                                                                                                                                    KLINGER, KATHERINE W
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 Release #1.0,
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 Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47;
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-17.8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 53526 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-658-136-2
Search completed: October 12, 2000, 17:41:13 Job time: 30037 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 4.1%; Score 50.6; DB 5; Length 53526; Best Local Similarity 50.6%; Pred. No. 0.025; Matches 122; Conservative 0; Mismatches 119; Indels 0;
                                                                                                                                                                                                                  34693 GGAGGGAGGAGGGAGGAGGAGGAGGAGGAGGAGGAGGGAGGAGGAGGAGGAGGAGGAGGAGGA
                                                                                                                        34513 A 34513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
FILING DATE:
                                                                                                                                                                                                                                                        243 gggacatgtgtaggtatcggcacaactatccggatctggtggaacgagactgcaatgggg 302
                                                                                                                                                                                                                                                                                                                                                  183 cggcgcggcccagctcgttccagtccagaatgacagggtccagaaactggcgagccacga 242
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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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GenEmbl:*

1: gb_bal:
2: gb_bal:
3: gb_om:*
4: gb_om:*
5: gb_pl:
6: gb_pl:
6: gb_pl:
7: gb_pl:
10: gb_pl:
11: gb_r
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2250
1 tgggctcagccacg
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Gapop 10.0 , Gapext 1.0
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                                 9b_bal:
9b_on:
9b_on:
9b_on:
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9b_pl:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2 (bases 1 to 2208)
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2 agon, I.S., Verderame, M.F., Allen, S.S. and McLaughlin, P.J. Direct Submission
Submitted (04-JUN-1999) Neuroscience and Anatomy, Penn Stauniversity College of Medicine, 500 University Drive, Hers
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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109027 Sequence 3
M11926 Plasmodium
10848 Sequence 1
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106498 Plasmodium
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AC069257 Homo sapi
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U90353 Strongyloid
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Direct Submission
Submitted (26-JUL-1999) Department of Pennsylvania State University College Drive, Hershey, PA 17033, USA
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Zagon, I.S., Verderame, M.F., Allen, S.S. and McLaughlin, P.J. Cloning, sequencing, chromosomal location, and function of encoding an opioid growth factor receptor (OGFr) in humans brain Res. 856 (1-2), 75-83 (2000)
                                                                                               Submitted (26-JUL-1999) Department of Pennsylvania State University College Drive, Hershey, PA 17033, USA Location/Qualifiers
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/protein_id="Asf64403.1"
/db_xref="0;1795301"
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/translation="MDDPDCDSTWEEDEEDAEDAEDECEDGEAAGARDADAGDEDEE
SEEPRAARPSSEQSRWIGSRWWRAITROWCRYRHMYPDLYERDCNODTPHLSFYRNEIR
FLPNGCFIEDLIQHWYDNYDLLEDNHSYIGWLFPLREGOVNWHARCHTIREUVEKSS
OEIOERLVRAYELMLGFYGIRLEDRGTGTVGRAQNYQKRFQNLNWRSHNNLRITRILK
SPCELSLEHFGAAFLWEFFLESTLVRRELDGVRQSALDYWFAVRCHQRRQLVHFAWE
HERPRKCKFYWGFDGULAWFKSSLPHFLEGSRKYLEEGGSPGDDDHEASTGGRTCGPEH
SKGGGRVDEGPQFRSVEFQDAGFLERSOGDEAGGHGEDRPEFLSPKEKKRKLELSRR
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Zagon, I.S., Verderame, M.F., Allen, S.S. and McLaughlin, P.J.

Cloning, sequencing, chromosomal location, and function of
encoding an opioid growth factor receptor (OGFr) in humans

Brain Res. 856 (1-2), 75-83 (2000)
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AF172453.
 Submitted (26-JUL-1999) Department of Neuroscience Pennsylvania State University College of Medicine,
                               Zagon, I.S., Verder Direct Submission
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/db_xref="oqi-795307"
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/translation="mdDpCDSTWEEDEEDAGRACNYPEDAGRACHTRETYRIK
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HERPRCKFVWGPQDKLRFEKPSSLPHPLEGSRKVEEEGSPGDPDHEASTOGRTCEPEH
SKGGGRVDEGTQPRSVERDDAGFLERSGGDEAGGHGEDREEDLSFKESKRKLELSGR
EQPPTGPGPQSASTVEKIALMLEGCALSGGSLRTGTGEVGQODGEAVQPCRQDLGAR
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GFKGGTPGSPSETPGDSAAVASGAQDEPAKTPSETPGFSPAGFTRDEPAESPSETPGFR
AGPAGDEPAESPSETPGPRAGPAGDEPAKTPSETPGFSPAGFTRDEPAESPSETPGFR
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alternatively spliced"
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AF109134.1 G
Liu,J., Brewton,R.G., Takanosu,M., Wood,B.M. and Mayne,R. Direct Submission
Submitted (23-NOV-1998) Cell Biology, University of Alabama at Birmingham, 1670 University Blvd. VH302, Room 605, Birmingham,
                                                                                                Liu,J., Brewton,R.G., Takanosu,M., Wood,B.M. and Mayne,R. Cloning of 7-60: A human gene from chromosome 20q13.3 which a novel intracellular protein motif repeated seven times
                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2423)
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LPNGCFIEDLIONWTDNYDLLEDNHSYTOWLFFLREPGYWHAKRLTLREVEVFKSSQ
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LGELGLLEHQAPELVRFFLEESLVRRELPGVRQSALDYFWFAVGCHRORDCHFAWEH
FRENCKFYWGPQDKLRRFKPSSLPHPLEGSRKVEEEGSPGDPDHEASTQGRTCGPEHS
KGGGRVDEGPQRSVEPODAGPLERSQGDEAGHGEDRPEPLSFKEKKRKLELSRRE
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PKEGTTGSPSETFGPSPAGPAGDEPAESPSETFFPRPAGPAGDEPAESPSETFGPRPA
GPAGDEPAKTPSETFGPSPAGPAGDEPAESPSETFGPRPAGPAGDEPAESPSETFGPRPA
GPAGDEPAKTPSETFGPSPAGPAGPTRDEPAKAGEAAELQDAEVESSAKSGKP"
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/db_xref="taxon:9606"
/chromosome="20"
/map="20q13.3"
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/protein_id="AAD03737.1"
/db_xref="GI:4139228"
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70.7%;
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Pred. No. 4.6e-140;
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            agagaatcactcctacatccagtggctgtttcctctgcggggaaccaggagtgaactggca
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                                                                aaatggggctctcatcgaggacattcttcagaactggaaagacaactatgacctcctgga
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                                                  CTGCGACTCCACCTGGGAGGAGGACGAGGAGGAGGATGCGGAGGACGAGGACTG 107
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1 (bases 1 to 1232)

Zagon, I.S., Verderame, M.F., Allen, S.S. and McLaughlin, P.J.

Cloning, sequencing, chromosomal location, and function of encoding an opicid growth factor receptor (OGFr) in humans brain Res. 856 (1-2), 75-83 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pennsylvania State University
Drive, Hershey, PA 17033, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="opioid growth factor receptor"
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GEIQERLYRAYELMLGFYGIRLEDRGTGTVGRAQNYGKRFQNLNWRGSHNNLRITRILK
SPCELSLEHFQAPLVERFLESTLYRRELPGVRQSALDYFMFAVRCRHGRRQLVHFAWE
HFRPRCKFVWGFQDLVLRFKPSSLPHFLEGSRRVEEEGFAGDEPAESPSETPGFSPAG
FTRDEPAKAGEAEACCLAVSSHPALPCAPVFVNRPFWSGGRRAGLAFLSLMPSKAFSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alternatively
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alternatively spliced"
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/db_xref="taxon:9606"
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/clone="127"
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76.5%;
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Primates;
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Pred. No. 1.2e-1
0; Mismatches 2
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                                                                                                                         requests: clonerequest(sanger.ac.uk
On Jul 8, 2000 this sequence version replaced 9:8919619.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
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feature key.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human DNA sequence from 20q13.2-13.33, complete AL035669 AL035669.43 GI:8979786
                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (09-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial cione contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 mapping Group. Further information can be found at
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533. .4822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18320. .18495

/note="44 copies 4 mer acac

18321. .18496

/note="11 copies 16 mer 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="6 copies 38 mer 98% conserved"
7892. 8074
/note="MER68A repeat: matches 68. .210 of consens:
8674. .8966
note="Ally repeat: matches 5. .296 of consensus"
                                                                                                                                /note="25 copies 2 mer ac 72% conserved"
19329. .19433
/note="LTR16C repeat: matches 286. .387
                                                                                                                                                                                                                                                /note="9 copies 18 mer
18327. .18486
                                                                                                                                                                                                                                                                                                                                                                                                        /note="4 copies 48 mer 67% conserved" 18317. 18496 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 18486 // 18319. 1
note="4 copies 20 mer
                                                                                   note="4 copies 34 mer
                                                                                                                                                                                                                        'note="8 copies 20 mer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="5 copies 40 mer 66% conserved"
18307. .18498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="9 copies 33 mer 66% conserved"
16585. 16840
/note="16 copies 16 mer 66% conserved"
16586. 16875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="44 copies 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="5 copies 48 mer 73% conserved"
16603. .16842
/note="3 copies 80 mer 77% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="5 copies 58 mer 72% conserved"
16590. 16874
'note="15 copies 19 mer 64% conserved"
16593. 16872
'note="7 copies 40 mer 67% conserved"
16598. 16837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="MER5A repeat: matches 35. .165 of consensus"
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.e="17 copies 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e="AluSq repeat: matches 1.
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                   '2 copies 74
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                                                                  .19604
                                                                                                                  .19590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .16891
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                                          mer
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76% conserved"
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Query Match
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les 596; Conser
                                                                                                                                                                                                                                                                                                                                                                                                               GAGCTGCCGGGGTGCGGCAGAGTGCCCTGGACTTCATGTTCGCCGTGCGCTGCCC
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                                               tgtctctgaggtagagaaaattgcccttaaccttgaggagtgtgcccttagccctatcag
                                                                                                                gaaaaggaagttggaggggaacaggcaggagcaggtcccaggggaggcagatccccaggg 1307
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                                                                                                                                                                                                                                                                       cacccagggtcggacctgtggatctggaagggacctgagtggggacagtggaacagctga
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                                                                                                                                                                                                                                                                                                                                                               CGTCTGGGGGCCCCAAGACAAGCTGCGGAGGTTCAAGCCCAGCTCTCTGCCCCATCCGCT
                                                                                                                                                                                                                                                                                                                                                                             tgtctgggggccccgtgacaagctgcggagattcaagccccagaccataccccagccact 1031
CCTCAGGACGGGGACCCAGGAAGTGGGCCGTCAGGACCCCTGGGGGAGGCAGTGCAGCCCTG
                                                                                                                                                     ggatgaag-----
                                                                                                                                                                                                       GGGGCCCCAGCCACGGAGCGTGGAGCCCCAGGATGCGGGACCCCTGGAGAGGAGCCAGGG
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                                                                                                   GAAGAGGAAGCTGGAGCCGGCGGGGAGCAGCCGCCCACAGAGCCAGGCCCTCAGAG
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20704 .20805
/note="3 copies 34 n
20710 .20811
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/note="5 copie
21349 .21410
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21584. .2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="2 cor' 20722
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25853. .26065
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/note="LTR16A repeat: matches 88. .158
21779. .21852
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24787. .24847
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Pred. No. 9e-65;
D; Mismatches 229;
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AUTHORS
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SOURCE
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ORIGIN
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Best Local Sim
Matches 590;
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                  cacagccacaacctgcgtattacacgcatcctcaagtcactgggtgagctgggctta
CGCAGCCACAACCACCGCATCACACGCATCCTCAAGTCGCTGGGTGAGCTGGGCCTC 4950
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Mammalia; Eutheria; P
1 (bases 1 to 6670)
Takanosu,M., Liu,J. a
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Submitted (10-DEC-1998) Cell Biology, University of Alabama
Surmingham, VH 302, Room 605, Birmingham, Alabama 35294, US
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AF112980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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                                                                                     Similarity
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                                                                      Conservative
                                                                                                                                                                                                                                            /protein_id-"AAD03745.1"
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1998 c 2169 g 1136 t
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                                                                  Score 329.4; DB 11;
Pred. No. 3.3e-63;
0; Mismatches 231;
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Nephila clavipes.

Nephila clavipes

Rephila clavipes

Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Aranea

Araneomorphae; Entelegynae; Araneoidea; Tetragnathidae; Nephil.

1 (bases 1 to 2830)

Hayashi,C.Y. and Lewis,R.V.

Evidence from flagelliform silk cDNA for the structural basis elasticity and modular nature of spider silks

J. Mol. Biol. 275 (5), 773-784 (1998)
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2 (bases 1 to 2830)
Hayashi, C.Y. and Lewi
Direct Submission
                      AF218621S1 14999
Nephila clavipes :
partial cds.
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Hayashi,C.Y. and Lewis,R.V.
Molecular architecture and evolution of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae; Araneomorphae; Entelegynae; Araneoidea; Tetragnathidae; Nephila. (bases 1 to 14999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nephila clavipes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (22-DEC-1999) Molecular Biology, University of Wyoming. P.O. Box 3944, Laramie, WY 82071, USA
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Hayashi,C.Y. and Lewis,R.V
Direct Submission
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                                   GAGPGGAGPGGAGGAGGAGGAGGSGGAGGSGGTTIIEDLDITIDGADGPITISEELII
SGAGGSGPGGAGPGGVGPGGSSGPGGVGPGGSGGPGGVGPGGSGAGGPYGPGGA
GSGPGGAGGAGGPGGAYGPGGSYGPGGSGGPGGAGGPYGPGGAGGPYGPGGAG
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10216. .11544,12973.
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10216. .11544,12973. .>14211)
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McCutchan, T.F., Lal, A.A., De la Cruz, V.F., Miller, L.H., Maloy, W.L.
Charcenvit, Y., Beaudoin, R.L., Guerry, P., Wistar, R.Jr.,
Hoffman, S.L., Hockmeyer, W.T., Collins, W.E. and Wirth, D.F.
Sequence of the immunodominant epitope for the surface protein on
sporozoites of Plasmodium vivax
Science 230, 1381-1383 (1985)
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J02751 M12137
J02751.1 GI:160172
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                                                                                                                                                                                        /dev_stage="infective sporozoite stage"
/country="El Salvador: La Paz"
/note="draft entry and computer-readable sequence kindly
provided by V.F.de la Cruz, 30-MAR-1987"
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/protein_id="AAA29529.1"
/db.xref="Gi:552192"
/translation="NGVNFNNVDASSLGAAHVGQSASRGRGLGENPDDEEGDAKKKKD
                                                                                                                                                                        /codon_start=2
                                                                                                                                                                                                                                                                                                   /clone-"pPv1"
                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:5855"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (15-APR-1994) Allen Saul, Queensland Insitute of Medical Research, 300 Herston Road, Brisbane, Queensland, 4029, Australia
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/rpt_type=tandem
/rpt_unit=185. .211
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/db_xref="taxon:5855"
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Local Similarity 57.7%;
les 135; Conservative
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                                                      Burton, J
                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                              SEQUENCING IN PROGRESS AL139384
                                                                                                                                                                                                                                                                Homo sapiens chromosome
                                                                                                                                                          Direct Submission
                                                                                                                                                                                                         Homo sapiens
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HTG; HTGS_PHASE1; HTGS_DRAFT
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RP11-88E10 map q33.1-34, ***
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1.5e-06;
hes 99;
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/organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="13"	Location/Qualifiers 1209266	gap of 100 bp in 1	194650: contig of 194750: gap of	186878: contig of 186978: gap of	5 170220: contig of 1 170320: gap of	168335: contig of 168435: gap of	5 164677: contig of 2313 bp in] 8 164777: gap of 100 bp	5 162364: contig of 1356 pp in 1	7 160808: contig of 9462 bp in 1 9 160908: gap of 100 bp in 1	56 151246: contig of 47 151346: gap of	58 142255: contig of	ו בו מ	7 132450: contig of	8 130776: contig of 7 130876: gan of	110517: contig of 110617: gap of	100259: contig of	84390: contig o	* 69142 78379; contig of 9238 bp in length * 78380 78479; gap of 100 bp	69041: contig of 11	2	44470: gap of 100 53937: contig of 94	0: contig of 16101 bp in	28169: contig of 1314	26755: contig of	24518: contig of 4	19850: contig of	1 17023: contig 17024: contig	on as it is available and the accession n	s of N, but the exact sizes of the secord will be updated with the	n and their order in this sequence Gaps between the contigs are repre	This is a 'working draft' sequence. It currentles of 27 contigs. The true order of the pieces	n 020 ba	size: 206666; sum-of-cor	Consensus quality: 197814 bases at least Q30 Consensus quality: 202387 bases at least Q20
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Nephila madagascariensis f
upstream partial cds.
AF218623
AF218623.1 GI:7106226
                                                                                                                                                                                                                                                                                 2 (bases 1 to 14355)
Hayashi,C.Y. and Lewis,R.V.
Direct Submission
Submitted (22-DEC-1999) Molecular Biology, University of Wyoming, P.O. Box 3944, Laramie, WY 82071, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                            protein gene
Science 287 (5457), 1477-1479 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                         Nephila madagascariensis.

Nephila madagascariensis

Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Araneomorphae; Entelegynae; Araneoidea; Tetragnathidae; Nephila.

1 (bases 1 to 14355)

Hayashi,C.Y. and Lewis,R.V.

Molecular architecture and evolution of a modular spider silk
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/db_xref="taxon:115969"
join(<1. .845,3466. .3864,4381. .5739,7062. .8078,9528. .10814,
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Pred. No. 2e-06;
0; Mismatches 86;
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BASE COUNT ORIGIN

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Query Match
                                                                       10625 TACGGACCGGGTGGTGCAGGTGGACCCTACGGACCAGGTGGTGCAGGTGGACCCTACGGA 10684
                                                                                                           10565 GGAGGTGAAGGACCCGGTGGTGCTGGTGGACCCTACGGACCTGGAGGTGCAGGTGGACCC 10624
                                                                                                                           1557 ggactcaaacagccaggttggggcagaggattccaaaagccaggtggggccggaggatcc 1616
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           cgggccagaggacccaaacagccaggtggtg 1767
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                                                                                   aaacagccaggtggggctggaggacccaaacagccaggtcgggccagagggacccaaacag 1676
GGTGCTGGTGGACCCTACGGACCTGGAGGTG 10775
                                  CCAGGTGGAGCAGGTGGACCCTACGGACCGGGTGGTGGTGGTGGACCCTACGGACCGGGT 10744
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Search completed: October 14, 2000, 05:00:16 Job time: 8208 sec

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             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
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6: /cgn2_6/ptodata/2,
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/cgn2_6/ptodata/2/ina/5D_COMB.seq:*
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/cgn2_6/ptodata/2/ina/6CTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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                                US-08-232-463-14
US-08-479-537A-1
US-08-479-537A-2
US-09-130-114-2
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US-09-130-114-15
US-09-130-114-15
US-08-087-783A-15
US-08-087-783A-15
US-08-08-770-379-17
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27 54 2.4 1091 2 US-08-452-531-1 Sequence 1, Appli 29 54 2.4 1091 2 US-08-460-746A-1 Sequence 1, Appli 30 50.8 2.2 2277 2 US-08-676-957-2 Sequence 2, Appli 30 50.8 2.2 2277 2 US-08-676-947-2 Sequence 2, Appli 31 50.8 2.2 2277 4 US-08-676-914-2 Sequence 2, Appli 32 50.8 2.2 2301 2 US-08-691-83 Sequence 2, Appli 33 50.8 2.2 2301 2 US-08-958-136-2 Sequence 2, Appli 35 50.6 2.2 53526 5 US-08-58-136-2 Sequence 7, Appli 20 50.6 2.2 53576 5 US-08-691-36-2 Sequence 7, Appli 21 50.6 2.2 53577 5 US-08-658-136-2 Sequence 7, Appli 21 50.6 2.2 53577 5 US-08-658-136-1 Sequence 1, Appli 39 48 2.1 1052 2 US-08-658-136-1 Sequence 1, Appli 40 48 2.1 1052 2 US-08-468-065-1 Sequence 1, Appli 41 42 48 2.1 1052 3 US-08-468-065-1 Sequence 1, Appli 42 48 2.1 1052 3 US-08-468-065-1 Sequence 1, Appli 42 48 2.1 1052 5 US-08-468-065-1 Sequence 1, Appli 42 44 47.4 2.1 496 2 US-08-263-413-23 Sequence 1, Appli 44 47.4 2.1 496 2 US-08-263-413-23 Sequence 1, Appli 5 Sequence 1, Appli 6 Sequence 2, Appli 6 Sequence 3, Appli 6 Sequence 2, Appli 6 Sequence 3, Appli 6 Sequence 3, Appli 6 Sequence 4 Sequence 4 Sequence 5, Appli 6 Sequence 6 Sequence 6 Sequence 6 Sequence 7 Sequence 8 Seque
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TELEFAX: (703)683-4109

TELEX: 899149

INFORMATION FOR SED ID NO: 14

SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZ9pt-F1s
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                            APPLICATION NUMBER: EP 91 114
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-3300
                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                          TELEPHONE: (703)000
TELEPHONE: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road,
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 22313-0299
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Best Local S
Matches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: CHAMBON
APPLICANT: KIENY,
APPLICANT: LATHE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08479537A Patent No. 5861381
                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 90/13101

FILING DATE: 23-OCT-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/FR91/008

FILING DATE: 23-OCT-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/039,320

FILING DATE: 04-APR-1993
                                                                                                                                                                                                                                                                                                             ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                          COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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 FRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                942
                                                                                                                                                                                        APPLICATION NUMBER: US/O FILING DATE: 07-JUN-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                  COUNTRY: United States ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                     STREET: P.O. Box CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gaagaggaagctggagctgagccggcgggagcagccgcccacagagccaggccctcagag 1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ggggccccagccacggagcgtggagccccaggatgcgggacccctggagaggagccaggg 1121
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                                                                                                                                                                                                                                                                                                                                                                                                                      P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KIENY, Marie-Paule
LATHE, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.3%; Score 76; DB 1; Length 7218; ilarity 6.0%; Pred. No. 4.3e-07; Conservative 240; Mismatches 155; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAMBON, Pierre
                                                                                                                                                                                                                                                                                                                                                                                                                                        BURNS, DOANE, SWECKER & MATHIS, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHARMACEUTICAL COMPOSITION TREATMENT OR PREVENTION OF
                                                                                                                                                                                                                                                              Release #1.0,
                                                                                                      WO PCT/FR91/00835
                                                                                                                                                                                                                           US/08/479,537A
US 08/403,576
                                                                                                                                                                                                                                                              Version
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COATION: 496
COTHER INFORMATION:
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US-08-479-537A-1
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6192 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                 1705
                                                                                                                                                                                                                                    1645
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                 581
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: /note- "The nucleotides spanning OTHER INFORMATION: 439-5239 constitute a repeated region wherein the reOTHER INFORMATION: nucleotides and encodes 20 amino acids, 17 of which OTHER INFORMATION: The number of such repeats varies from 1 to 80."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: repeat_region LOCATION: 496
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LOCATION:
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CCCACGGTGTCACCTCGGCCCCGGACNNNAGGCCGNNNCCGGGCTCCACCGCCCCCNNNG 760
                                                                                                                                                                                                                                                                                                                                  161;
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121..6166
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58..120
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836-2021
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which is the codon for Pro or Ala wherein Pro =
or CCG; and Ala = GCT, GCC, GCA, or GCG."
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which is the codon for Thr or Asn wherein
or ACG; and Asn = AAT or AAC."
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Pred. No. 4.6e
0; Mismatches
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1.6e-07;
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US-08-479-537A-4
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APPLICANT: CHAMBON, Pierre
APPLICANT: KIENY, Marie-Paule
APPLICANT: LATHE, Richard
APPLICANT: HAREUVENI, Mara
                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703) 836-20 INO:
                                                                                                                                                                     NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FR 90/13101 FILING DATE: 23-OCT-1990 PRIOR APPLICATION DATA:
                                                                     NAME/KEY: repeat_region
LOCATION: 439.5239
OTHER INFORMATION: /note=
OTHER INFORMATION: 439-52
OTHER INFORMATION: nucleo
                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08
FILING DATE: 04-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGI
                                       FEATURE:
                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 07
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: WO PCT/FR91/00835 FILING DATE: 23-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/479,537A FILING DATE: 07-JUN-1995
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                 NAME/KEY:
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LOCATION:
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P.O. Box 1404
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836-2021
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                                               /note= "The nucleotides spanning 439-5239 constitute a repeated region wherein the repeat is (nucleotides and encodes 20 amino acids, 17 of which are fixed the number of such repeats varies from 1 to 80."
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; LENGTH: 1931
; TYPE: DNA
; ORGANISM: EBNA
US-09-130-114-2
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                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Horlick, Robert A.
APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing
TITLE OF INVENTION: From Multiple Transfected Episomes
FILE REFERENCE: 0867/1D903US1
                                                                                                                                                                                                                                                                  Sequence 2, Application US/09130114 Patent No. 5976807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.3%;
Best Local Similarity 45.5%;
Matches 161; Conservative
                                                                 SOFTWARE: FastSEQ
SEQ ID NO 2
                                                                                                CURRENT APPLICATION NUMBER: US/
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 36
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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                                                                                  for
                                                                                 Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Nucleotide 496 is X2 = NNN
which is the codon for Pro or Ala wherein
or CCG; and Ala = GCT, GCC, GCA, or GCG."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Nucleotide 457 is X1 = NNN
which is the codon for Pro or Ala wherein
or CCG; and Ala = GCT, GCC, GCA, or GCG."
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                                                                                                                               us/09/130,114
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Pred. No. 4.6e-07;
D; Mismatches 193
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Query Match
Best Local Similarity

3.3%;

Score 74.6; DB 4; Pred. No. 6.4e-07;

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US-09-050-863-2
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                                                                                                                                     Query Match
Best Local Similarity
Matches 229; Conserv
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TELEPHONE: (415) 781-1989
TELEPAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2580 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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APPLICANT: Hiang, Betty
APPLICANT: Payan, Don
TITLE OF INVENTION: Mammalian Protein Interaction Cloning
TITLE OF INVENTION: System
NUMBER OF SEQUENCES: 5
CORRESPONDENCES: 5
1073 cacggagcgtggagccccagggatgcggggacccctggagaggagccaggggggatgaggcag 1132
                                                                1016
                                                                                                                                                                                                            STRANDEDNESS: unl
TOPOLOGY: unknown
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: CA
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Silva, ROBIN M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-
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                                                                                                                956
                                        767
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                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 30-MAR CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                          ggacctgtgggccagagcatagcaagggtgg---gggcagggtggacgaggggccccagc 1072
                                                                                                      ggaaggtggaggaaggaagccccggggacccccgacgaggccagcacccagggtc 1015
                                     GTGACGGAGGAGCTGGGGGCCGGAGGTGGAGGACGAGGACGGGGAGGACGAGGACGGAGGAG
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4 Embarcadero Center,
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ilarity 47.7%;
Conservative
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                                                                                                                                    Score 67.2; DB 5;
Pred. No. 2.1e-05;
0; Mismatches 248;
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SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 1 LENGTH: 5452 TYPE: DNA CORGANISM: VEBNA US-09-130-114-1
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US-09-130-114-1/c
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Best Local Similarity
Matches 229; Conserv
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APPLICANT: Damaj, Bassam B.
APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing
TITLE OF INVENTION: From Multiple Transfected Episomes
FILE REFERENCE: 0867/11093US1
CURRENT APPLICATION UNMER: US/09/130,114
CURRENT APPLICATION UNMER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 36
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                          tggagaagatcgctctgaatttggaggggtgtgccctcagccagggcagcctcaggacgg
9999ccac9999aa9ata99cc99a9cccttaa9ccccaaa9a9a9caa9aa9a9gaa9c 1192
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                                                                                                                                tgggagccagggtggccgacaaggtgaggaagcggaggaaggtggatgaaggtgctgggg 1432
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Pred. No. 2.4e-05;
0; Mismatches 248;
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US-07-884-811-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.9%;
Best Local Similarity 47.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                   1073
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                                                                                                                                                                                                                                                                                                                                    1016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch,
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CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TORNEI A PROGRET Ginger R.
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REGISTRATION NUMBER: 755.1
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: UPPLICATION NUMBER: UPPLIC
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                                                                                                                                                                   cacggagcgtggagccccaggatgcgggacccctggagaggagccaggggggatgaggcag 1132
                                                                                                                                                                                                                                                                                                                         ggacctgtgggccagagcatagcaagggtgg---gggcagggtggacgaggggccccagc 1072
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South San Francisco
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    Paul J. Lokker, Nathalie A. Mark, Melanie R
SINGLE-CHAIN HEPATOCYTE GROWTH FACTOR VARIANTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 67.2; DB 1;
Pred. No. 2.8e-05;
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415/ysz TELEFAX: 415/ysz TELEX: 910/371-71.68
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10596 bases
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5328837
GENERAL INFORMATION:
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                                           1016 ggacctgtgggccagagcatagcaagggtgg---gggcagggtggacgaggggccccagc 1072
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
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                                                                                                                                                                                                                                                 Score 67.2; DB 1;
Pred. No. 2.8e-05;
0; Mismatches 248
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                                                                                                                                                                                                                                                    248;
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US-08-087-783A-15
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; Sequence 15, Application US/08087783A
; Patent No. S547856
; PATENT NO. STATION:
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                                                                TELEPHONE: 415/225-5416
TELEPAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                  APPLICATION NUMBER: 07/8848
FILING DATE: 18-MAY-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/8859
FILING DATE: 18-MAY-92
ATTORNEY/AGENT INFORMATION:
NAME: MATSCHANG, Diane L.
REGISTRATION NUMBER: 35,600
                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: WinPatin (Ge
CURRENT APPLICATION DATA:
                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: GOGOWSK1, Paul J., LOKKEY, TITLE OF INVENTION: HEPATOCYTE GROWTH NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
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                      LENGTH: 10596 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                            REGISTRATION NUMBER: 35,600 REFERENCE/DOCKET NUMBER: 90
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
                TOPOLOGY:
                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
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Query Match

2.98;

Score

67.2;

DB 1;

Length 10596;

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RESULT 10
US-08-194-088B-15
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Matches 229; Conservative
             TELEFAX: 415/952-98
TELEX: 910/371-7168
INFORMATION FOR SEQ ID N
                                                                                           CLASSIFICATION: 530
PRIOR APPLICATION DATA:
RAPPLICATION UNMAER: 07/8848
FILING DATE: 18-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gallegos, R. Thomas
REGISTRATION NUMBER: 32,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                       REFERENCE/DOCKET NUMBER: 75
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-2614
TELEPEAX: 415/952-9881
                                                                                                                                                                                                                        SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 5.25 in
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                            APPLICATION NUMBER:
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Bruno
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0; Mismatches 248; Indels
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RESULT 11
US-08-194-087-15
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-194-088B-15
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                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: GODOWS!
                                       APPLICATION NUMBER: US/01
FILING DATE: 18-MAY-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                         2707
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb
                                                                                                                                                                                                                                                                                            APPLICANT: GODOWSKI, Paul J. LOKKER, TITLE OF INVENTION: HEPATOCYTE GROWTH NUMBER OF SEQUENCES: 21
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                           FILING DATE:
                                                                                                                                                                                                                                     CITY: South San Francisco
                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                     STREET:
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Pred. No. 2.8e-05;
0; Mismatches 248;
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RESULT 12
PCT-US93-04648-15
Sequence 15, Application PC/TUS9304648
GENERAL INFORMATION:
APPLICANT: Generatech, Inc., Godowski,
TITLE OF INVENTION: HEPATOCYTE GROWTH
NUMBER OF SEQUENCES: 21
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TELEPHONE: 415/225-3216
TELEPAX: 415/952-9881
TELEFAX: 910/371-7168
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 10596 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.9%;
Best Local Similarity 47.7%;
Matches 229; Conservative
          COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 1nch, 360 Kb |
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2347
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                                                                                                                           STREET: 460 Point San Bru
CITY: South San Francisco
STATE: California
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                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
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PCT/US93/04648
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                                                                    floppy
                                                                                                                                                                                                                    FACTOR VARIANTS
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FILING DATE:

19930517

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RESULT 13
US-08-770-379-17
; Sequence 17, Application US/08770379
; Patent No. 5849564
; Patent No. 5849564
                     APPLICANT: Chang, Yuan
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 10596 bases
TYPE: NUCLEIC ACID
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Best Local S
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              TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 18-MAY-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/885971
FILING DATE: 18-MAY-92
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  956 ggaaggtggaggaaggaagccccggggacccccgaccacgaggccagcacccagggtc 1015
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REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 755,779P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07,
FILING DATE: 18-MAY-92
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Local Similarity 47.7%;
hes 229; Conservative
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TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                          ggacccaggaagtgggcggtcaggaccctggggaggcagtgcagccctgccgccaacccc 1372
                                                                                                                                                                                                           tgggagccagggtggccgacaaggtgaggaagcggaggaaggtggatgagggtgctgggg 1432
                                                                                                                                                                                                                                                                       tggagaagatcgctctgaatttggaggggtgtgccctcagccagggcagcctcaggacgg 1312
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Pred. No. 2.8e-05;
0; Mismatches 248
           FROM
        KAPOSI'S SARCOMA-ASSOCIATED
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Sequence 1, Application US/07945283
Patent No. 5352596
GENERAL INFORMATION:
APPLICANT: Cheung, Andrew K.
APPLICANT: Westley, Ronald D.
TITLE OF INVENTION: Pseudorabies '
TITLE OF INVENTION: Involving The
                                                                                                          RESULT 14
US-07-945-283-1
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Andrew K.
Ronald D.
Pseudorables Virus Deletion Muta
Pseudorables Proving The EPO and LLT Genes

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; STRANDEDNESS:
; TOPOLOGY: line
; MOLECULE TYPE: D
US-08-770-379-17
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Best Local Similarity 49.8%;
Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
ATTORNEY, AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 5234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
24581 CCCCAGGAGCCCCGGCAGCACCCCAGGAGCCCC 24613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 35100 base pairs
TYPE: nucleic acid
                                                                                                             24521
                                                                                                                                                                                                                                      24341
                   1887 atcggagaccccaggccccaggccgggacc 1919
                                                                          1707 atcggagaceccaggcccggcaggacctacaagggatgagccagccggcgagagccc 1766
                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: HERPESVIRUS, DNA INVASER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/770,379
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MEDIUM TYPE: Floppy disk
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CITY: New York
STATE: New York
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                                                   U.S.A.
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Pred. No. 6.8e-05;
0; Mismatches 167
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NUMBER OF SEQUENCES:

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Best Local :
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LOCATION:
FEATURE:
5716
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NAME: Ribando, Curtis P
REGISTRATION NUMBER: 27976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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ADDRESSEE: Curtis P. Ribando
STREET: 1815 No. 5352596th University Street
                                                                                                  LOCATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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MEDIUM TYPE: Floppy
                                               FEATURE:
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                       183
                                                                         123
                                                                                                              63 ggaggaggacgaggaggatgcggaggacgcgggaggacggaggactgcgaggacggcgaggc 122
                                                                                                                                                  7 Match 2.7%;
Local Similarity 67.4%;
les 87; Conservative
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CITY: Peoria
                                                                                                                                                                                                                                            NAME/KEY:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                  ggcgcggcc 191
                                                               GTCGCTGCC 5724
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DEDNESS: double
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Pred. No. 0.00033;
0; Mismatches 42;
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RESULT

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Search completed: October 12, 2000, 17:36:25 Job time: 29749 sec

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US-08-728-323A-1
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                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 107; Conserv
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APPLICANT: Chang, Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STREET: LICC
STREET: New York
STATE: New York
STATE: U.S.A.
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MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
1208 AGGAG 1212
                                                                   1088 AGGATGACGAGGAGGATGACGAGGAGGATGACGAGGATGACGAGGAGGATGACGAGG 1147
                                                                                                                                                                                                      1028 AGGATGACGAGGATGACGAGGAGGATGACGAGGATGACGAGGAGGATGACGAGG 1087
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TITLE OF INVENTION:
                                                                                                    122
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                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 3489 base po
TYPE: nucleic acid
STRANDEDNESS: singl
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                               182 cggcg 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                    2 agaattcagcggccgctgaattctagccgagcatggacgaccccgactgcgactccacct 61
                                                                                                                                                      gggaggaggacgaggatgcggaggacgcggaggacgaggactgcgaggacggcgagg 121
                                                                                          ccgccggcgcgagggacgcggggacgaggacgaggagtcggaggagccgcggg 181
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1185 Avenue of the Americas
                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                         0;
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Pred. No. 0.00058;
0; Mismatches 78;
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                                                                                                                                                                                                                                                                                                         Length 3489;
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Minimum |
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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      Pred. No. is the number of results predicted by chance to I score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.
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length: 2000000000
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2408
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                             Copyright
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/6COMB.seq:*
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US-08-479-537A-1
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US-08-479-537A-1
US-09-130-114-2
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US-08-460-746A-2
US-08-460-746A-1
US-08-460-746A-1
US-08-460-555-1
US-08-676-967-5
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1389.877 Million cell updates/sec
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  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 45.4
Matches 215; Conservative
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LOCATION: 496
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 457
OTHER INFORMATION:
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IOCATION: 439..5339 The nucleotides spanning OTHER INFORMATION: /09-5239 constitute a repeated region wherein the reOTHER INFORMATION: nucleotides and encodes 20 amino acids, 17 of which OTHER INFORMATION: The number of such repeats varies from 1 to 80."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: repeat_region LOCATION: 439..5239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
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 CCCACGGTGTCACCTCGGCCCCGGACNNNAGGCCGNNNCCGGGCTCCACCGCCCCNNNG
                                                                CCCACGGTGTCACCTCGGCCCCGGACNNNAGGCCGNNNCCGGGGCTCCACCGCCCCCNNNG
                                                                                                              CCCACGGTGTCACCTCGGCCCCGGACNNNAGGCCGNNNCCGGGCTCCACCGCCCCCNNNG 760
                                                                                                                                                                                                                                                                                 CCCACGGTGTCACCTCGGCCCCGGACNNNAGGCCGNNNCCGGGCTCCACCGCCCCCNNNG 700
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121..6166
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which is the codon for
or CCG; and Ala = GCT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Nucleotide 487 is Y = NNN which is the codon for Thr or Asn wherein Thr = or ACG; and Asn = AAT or AAC."
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Pred. No. 2e-12;
0; Mismatches 2
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is the codon for Pro or Ala wherein
; and Ala = GCT, GCC, GCA, or GCG."
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GCC, GCA, or
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                          FEATURE:
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                                     NAME/KEY:
LOCATION:
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LOCATION:
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repeat_region 457
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APPLICATION NUMBER: FR 90/13101
FILING DATE: 23-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR91/00835
FILING DATE: 23-OCT-1991
PRIOR APPLICATION NUMBER: US 08/039,320
FILING DATE: 04-APR-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (703) 836-20
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
TOOLLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Teskin, Robin L.
REGISTATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01'
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,537A
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MEDIUM TYPE: Floppy
                                                           OTHER INFORMATION:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 07-JUN-
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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APPLICANT: KIENY, Marie-Pau
APPLICANT: LATHE, Richard
APPLICANT: HAREUVENI, Mara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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KIENY, Marie-Paule
LATHE, Richard
                                                                                                                                              repeat_region 439..5239
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58..120
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, 836-2021
-- NO: 4:
                                                      /note= "The nucleotides spanning 439-5239 constitute a repeated region wherein the renucleotides and encodes 20 amino acids, 17 of which The number of such repeats varies from 1 to 80."
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US-08-232-463-14/c

: Sequence 14, Application US/08232463

: Patent No. 5670367
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Best Local Similarity 45.4%;
Matches 215; Conservative
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GENERAL INFORMATION:
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NAME/KEY:
LOCATION:
                                                              APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKMER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER :
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     COMPUTER READABLE FORM:
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
                COUNTRY: USA
ZIP: 22313-0299
                                                     STREET: 1800 Dia
CITY: Alexandria
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LOCATION:
                                                                                                                                                                                                                                                                                                              CCCACGGTGTCACCTCGGCCCCGGACNNNAGGCCGNNNCCGGGCTCCACCGCCC
                                                                                                                                                                                                                                                                                                                                                                    CCCACGGTGTCACCTCGGCCCCGGACNNNAGGCCGNNNCCGGGCTCCACCGCCCCCNNNG
                                                                                                                                                                                                                                                                                                                                                                                           CCCACGGTGTCACCTCGGCCCCGGACNNNAGGCCGNNNCCGGGCTCCACCGCCCCCNNNG
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which is the codon for Thr or Asn
or ACG; and Asn = AAT or AAC."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Nucleotide 496 is X2 = NNN
which is the codon for Pro or Ala wherein
or CCG; and Ala = GCT, GCC, GCA, or GCG."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Nucleotide 457 is X1 = NNN
which is the codon for Pro or Ala wherein
or CCG; and Ala = GCT, GCC, GCA, or GCG."
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Pred. No. 2e-12;
0; Mismatches 2
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                                                                            US-09-130-114-2/c
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Sequence 2, Application US/09130114
Patent No. 5976807
GENERAL INFORMATION:
APPLICANT: HOTLICK, Robert A.
APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
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Best Local S
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APPLICATION NUMBER: EP 91 114
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
CLONE: pTZgpt-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  942 gctcgagggctccaggaaggtggaggaaggaaggccccgggggaccccgaccacgaggc 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
RRRRRRRRRRRRRRRRRRRRRATCGCAAGCTCCGACCTGCAGCCAAGCTCGG
                    cctcaggacggggacccaggaagtgggcggtcaggaccctggggaggcagtgcagccctg 1361
                                                                                                          tgcctcagaggtggagaagatcgctctgaatttggaggggtgtgccctcagccagggcag 1301
                                                                                                                                                                                      gaagaggaagctggagccggcgggagcagccgcccacagggccaggccctcagag
                                                                                                                                                                                                                                                                ggatgaggcagggggccacggggaagataggccggagcccttaagccccaaagagagcaa 1181
                                                                                                                                                                                                                                                                                                                                                  ggggccccagccacggagcgtggagccccaggatgcgggacccctggagaggagccaggg
                                                                                                                                                                                                                                                                                                                                                                                             cagcacccagggtcggacctgtgagccagagcatagcaagggtgggggggagggtggacga 1061
                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pTZgpt-F1s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.2%; Score 76; DB 1; Length 7218; Larity 6.0%; Pred. No. 2.8e-07; Conservative 240; Mismatches 155; Indels
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; LENGTH: 1931
; TYPE: DNA
; ORGANISM: EBNA
US-09-130-114-2
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i Sequence 17, Application US/08770379

Patent No. 5849564
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APPLICANT:
APPLICANT:
                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 5234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes TITLE OF INVENTION: From Multiple Transfected Episomes FILE REFERENCE: 0867/1D90US1 CURRENT APPLICATION NUMBER: US/09/130,114 CURRENT FILING DATE: 1998-08-06 NUMBER OF SEQ ID NOS: 36
                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Cooper &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
          STRANDEDNESS:
                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
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                       nucleic acid
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1185 Avenue of the
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Russo, James J
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linear
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Pred. No. 4.1e-07;
0; Mismatches 64;
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Americas
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DNA ENCODING S
                                                                                                                                                                                                                                             Version
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                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6114111 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
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NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                        APPLICANT: Lao, Ying APPLICANT: Hiang, Betty APPLICANT: Payan, Don
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1953
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                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FELECOMMUNICATION INFORMATION:
                                                                  APPLICATION NUMBER: FILING DATE: 30-MAR CLASSIFICATION:
                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                        ZIP:
                                                                                                                                                                                                                             STREET: 4 Embarcade:
CITY: San Francisco
            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAGGGGGATCCCGGCGCGCCCCCCCCCCGGAGGGGGATCCCGGCGCCC 24771
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                                                                                                                                                                                                                                                                                                                                                                                          Application US/09050863
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4 Embarcadero Cent
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                                                                              30-MAR-1998
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                                                                                                                                                                                                                                                                                    System
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48.2%;
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                                                                                         us/09/050,863
                                                                                                                                                                                                                                           Center,
            A-65638/DJB/RMS
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                                                                                                                                                                                                                                          Test, Albritton & Herbert
er, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 238;
                                                                                                                     Version #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3;
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TELEPHONE: (415) 781-1989
TELEPAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2580 base pairs

nucleic acid

unknown

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US-09-130-114-1/c ; Sequence 1, Application ; Patent No. 5976807
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                                                        ; TYPE: DNA; ORGANISM: VEBNA US-09-130-114-1
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Best Local Similarity
Matches 229; Conserv
                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Horlick, Robert A.
Query Match
Best Local Similarity
                                                                                                 SEQ ID NO 1
LENGTH: 5452
                                                                                                                         APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing
TITLE OF INVENTION: From Multiple Transfected Episomes
FILE REFERENCE: 0867/1D903US1
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT APPLICATE: 1998-08
CURRENT FILING DATE: 1998-08
NUMBER OF SEQ ID NOS: 36
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 3.0
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Score
Pred.
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Pred. No. 1.4e-05;
D; Mismatches 248;
67.2;
No. 1.
DB 4;
.7e-05;
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US-07-884-811-15
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Patent No. 5316921
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           TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEPAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                  OPERATING SYSTEM: PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBERS.
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SEQUENCE CHARACTERISTICS:
                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 75:
                                                                                                                                                      CLASSIFICATION: 530 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                         STREET: 460 Point San Bruno CITY: South San Francisco STATE: California
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FACTOR VARIANTS
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RESULT 9
US-07-885-971-15
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Best Local Similarity 47.7%;
Matches 229; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/885,97
FILING DATE: 19220518
                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
                                                                                                                                                   CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: GODOWSKI, Paul J. Lokker, TITLE OF INVENTION: HEPATOCYTE GROWTH NUMBER OF SEQUENCES: 21
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                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
STREET: 4
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STRANDEDNESS: single
TOPOLOGY: linear
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T: 460 Point San Bruno
South San Francisco
: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94080
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R.
33,055
                                                                                                                                                                                                                                                                                                                                                                                      360 Kb floppy disk
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RESULT 10
US-08-087-783A-15
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                                                                                                                                                                                                                                                          Sequence 15, Application US/08087783A Patent No. 5547856 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 10596 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.8%;
Best Local Similarity 47.7%;
Matches 229; Conservative
         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                            APPLICANT: Godowski, Paul J., Lokker, TITLE OF INVENTION: HEPATOCYTE GROWTH NUMBER OF SEQUENCES: 22
                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                                                                 2647
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TELECOMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEPHAX: 415/952-9881
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APPLICATION NUMBER:
                                                                                                                                     CITY: South San Francisco
STATE: California
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                                                                                                            ZIP:
                                                                                                                         COUNTRY:
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Pred. No. 2e-05;
0; Mismatches 248;
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NAME: MATSCHANG, DIANG L.

REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P075
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEPHONE: 415/952-9881
TELEPX: 910/371-7168
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:

P0755779P1

LENGTH: 10596 base pairs TYPE: Nucleic Acid STRANDEDNESS: Single

TOPOLOGY:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07
FILING DATE: 18-MAY-92

07/885971

PRIOR APPLICATION DATA:

FILING DATE: 1. CLASSIFICATION:

13-Jul-1993

FILING

APPLICATION NUMBER: FILING DATE: 18-MAN

18-MAY-92

07/884811

FILING DATE: 18-MAY-92 ATTORNEY/AGENT INFORMATION:

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RESULT 11

US-08-194-088B-15

Sequence 15, Application US/08194088B

Sequence 15, Application US/08194088B

Patent No. 5580963

GENERAL INFORMATION:

APPLICANT: GOGOWSKI, Paul J. Lokke:

TITLE OF INVENTION: SINGLE-CHAIN HEI

NUMBER OF SEQUENCES: 21
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Best Local Similarity 47.7%;
Matches 229; Conservative
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno
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Pred. No. 2e
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Application US/08194087

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RESULT 12
US-08-194-087-15
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Best Local Similarity 47.7%;
Matches 229; Conservative
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 07/8848
FILING DATE: 18-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gallegos, R. Thomas
REGISTRATION NUMBER: 32,992
REFERENCE/DOCKET NUMBER: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 income
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FILING DATE: 09-FEB-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
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                                                                  nucleic acid
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California
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SYSTEM: PC-DOS/MS-DOS
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US-08-194-087-15
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Best Local Similarity
Matches 229; Conserv
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                     1313 ggacccaggaagtgggcggtcaggaccctggggaggcagtgcagccctgccgccaacccc 1372
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                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 775
RELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: HEPATOCYTE GROWTH FACTOR PROTEASE DOMAIN VARIANTS NUMBER OF SEQUENCES: 21 CORRESPONDENCE ADDRESS: ADDRESSE: Genetech, Inc. STREET: 460 Point Co.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        956 ggaaggtggaggaaggaagccccgggggaccccgaccacgaggccagcacccagggtc 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 18-MAY-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: 5.25 inch, 360 Kb floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
tggagaagatcgctctgaatttggaggggtgtgccctcagccagggcagcctcaggacgg 1312
                                                                                                                                    9999ccac9g9gaagataggccggagcccttaagccccaaagagagcaagaagaagaggaagc 1192
                                                                                                                                                                                                                                                                          tggagctgagccggcgggagcagccgcccacagggccaggccctcagagtgcctcagagg 1252
                                                                                                                                                                                                                                                                                                                                             H: 10596 bases
nucleic acid
NDEDNESS: single
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South San Francisco
California
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47.7%;
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PCT-US93-04648-15
Sequence 15, Application PC/TUS9304648
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                        Best Loc
Matches
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TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                   2347
                                                                             1133
                                                                                                                                                                                                1016
1193 tggagctgagccggcgggagcagccgccacaggggccagggccctcagagtgcctcagagg
                                                2467
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                                                                                                                                       1073
                                                                                                                                                                                                                               2287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE, DOCKET NUMBER: 75:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07,
FILING DATE: 18-MAY-92
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 07/8
FILING DATE: 18-MAY-92
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Genentech, TITLE OF INVENTION: H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             956 ggaaggtggaggaaggaagccccggggaccccgaccacgaggccagcacccagggtc 1015
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                                                                                                                                                                                                                                                                                          Local Sin
hes 229;
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PFILING DATE: 1930517
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                                                                                                                                                                                         ggacctgtgagccagagcatagcaagggtgg---gggcagggtggacgagggggccccagc 1072
                                                                                                                                                                                                                           9999ccac9999aa9ata99ccggagcccttaa9ccccaaa9a9agcaagaagaggaagc 1192
                                                                                                      T: 460 Point San Bruno Blvd
South San Francisco
                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                     2.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
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Pred. No. 2e-0
0; Mismatches
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2e-05;
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US-07-945-283-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 309-685-4128
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                        TOPOLOGY: lin
MOLECULE TYPE:
HYPOTHETICAL: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cheung, A
APPLICANT: Wesley, F
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis P. Ribando
STREET: 1815 No. 5352596th University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2647
                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 309-685-4011 ext.513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: FEATURE:
                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 8438 base pairs
                            FEATURE:
                                                                                                                FEATURE:
                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                               ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDATE TO STREET: 10.
                                          NAME/KEY:
LOCATION:
                                                                                                                               NAME/KEY:
                                                                                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                                                                                                    ORGANISM:
                                                                                                                                                                                                                                                                                                                 TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ribando, Curtis P
REGISTRATION NUMBER: 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: UPFILING DATE: 19920911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
               NAME/KEY:
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622..6495
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             variation
                                          variation replace(1381,
                                                                                  replace(1267,
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                                                                                                                              replace(1099,
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replace(1566, "c")
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                                                                                                                                                                                                                                                                                                        double
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US-07-945-283-1
US-08-728-323A-1
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GENERAL INFORMATION: Chang, Yuan
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Best Local Similarity
                                                                                                                        TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                      PATE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
CLASSITETE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY:
                                      MOLECULE TYPE:
FEATURE:
                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Edelman, Isidore APPLICANT: MOOTE, Patrick S. TIITLE OF INVENTION: Immediat TITLE OF INVENTION: Sarcoma-TITLE OF INVENTION: Encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5716 GTCGCTGCC 5724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5656 GGCGGCGGCGGCGGGGGGCCCGGGGGGCGAGCGGCGGGCCGGGGAGAGGTCCGA 5715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 ggcgcggcc 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123
              NAME/KEY:
LOCATION:
                                                                                                LENGTH:
TYPE: n
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                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A. ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
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                                                                      TOPOLOGY:
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                                                                                            nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                     1185 Avenue
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Russo, James J.
                                                                      linear
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replace(7010, "g")
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                                                      DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immediate Early Protein From Kaposi's
                                                                                                                                                                                                                                                                                                                                                                                                                                        Dunham LLP of the Americas
                                                                                                                                                                                               0575/52268/JPW/MSC/SKS
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Pred. No. 0.00024;
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Search completed: October 12, 2000, 17:14:50 Job time: 28454 sec
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                                                                  1208 AGGAG 1212
                                                                                                                    1028 AGGATGACGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGATGACGAGG 1087
                                                                                          182 cggcg 186
                                                                                                                                       2 agaattcagcggccgctgaattctagccgagcatggacgaccccgactgcgactccacct 61
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Minimum
Maximum
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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US-08-479-537A-1
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                                                                                                                                                               MEDIUM TYPE: F10py disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,537A
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: FR 90/13101
FRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 90/13101
FILING DATE: 23-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR91/00835
FILING DATE: 23-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,320
FILING DATE: 04-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,576
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin BObit I.
      TELEFAX: (703) 836-2021 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: CHAMBON, Pierre
APPLICANT: KIENY, Marie-Paule
APPLICANT: LATHE, Richard
APPLICANT: HARBUYENI, Mara
TITLE OF INVENTION: TREATMENT OR
                                                                NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CITY: Alexandria
STATE: Virginia
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P.O. Box 1404
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US-08-658-136-1
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Best Local Similarity 45.4%;
Matches 188; Conservative
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OTHER INFORMATION:
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FEATURE:
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OTHER INFORMATION: /note= "The nucleotides spanning
OTHER INFORMATION: 439-5239 constitute a repeated region wherein the repeat
OTHER INFORMATION: nucleotides and encodes 20 amino acids, 17 of which are f
OTHER INFORMATION: The number of such repeats varies from 1 to 80."
FEATURE:
                                                                                                                                         1825
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LOCATION: 457
OTHER INFORMATION:
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STRANDEDNESS: single
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CCCACGGTGTCACCTCGGCCCCGGACNNNAGGCCGNNNCCGGGCTCCACCGCCC
                        ccatcggagaccccaggcccggccggcaggacctgcagggggacgaaccagcogagagc
                                                                                                                                                                                 CCCACGGTGTCACCTCGGCCCCGGACNNNAGGCCGNNNCCGGGCTCCACCGCCCCNNNG
                                                    CCCACGGTGTCACCTCGGCCCCGGACNNNAGGCCGNNNCCGGGCTCCACCGCCCCNNNG
                                                                                                           CCCACGGTGTCACCTCGGCCCCGGACNNNAGGCCGNNNCCGGGCTCCACCGCCCCCNNNG
                                                                                                                                  CCCACGGTGTCACCTCGGCCCCGGACNNNAGGCCGNNNCCGGGCTCCACCGCCCCNNNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or CCG; and Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Nucleotide 487 is Y = NNN which is the codon for Thr or Asn wherein Thr = ACT, ACC, or ACG; and Asn = AAT or AAC."
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which is the codon for
or CCG; and Ala = GCT,
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which is the codon for
or CCG; and Ala = GCT,
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Pred. No. 1
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Pro or Ala wherein
GCC, GCA, or GCG."
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Pro or Ala wherein Pro -
GCC, GCA, or GCG."
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIA Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,537A
FILING DATE: 07-JUN-1995
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 90/13101
FILING DATE: 23-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR91/00835
APPLICATION NUMBER: WO PCT/FR91/00835
FILING DATE: 23-OCT-1991
PRIOR APPLICATION NUMBER: US 08/039,320
ENLING DATE: 04-APR-1993
PRIOR APPLICATION NUMBER: US 08/039,320
ENLING DATE: 04-APR-1993
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Patent No.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: CHAMBO
                                                                                                                                                             FEATURE:
NAME/KEY:
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NAME/KEY: repeat_re
LOCATION: 457
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                   LOCATION: FEATURE:
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ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                     TOCATION: 439..5239 OTHER INFORMATION: /note= "The nucleotides spanning OTHER INFORMATION: /note= "The nucleotides spanning OTHER INFORMATION: 439-5239 constitute a repeated region wherein the repeat OTHER INFORMATION: nucleotides and encodes 20 amino acids, 17 of which are 10THER INFORMATION: The number of such repeats varies from 1 to 80."
                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAREUVENI, Mara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KIENY, Marie-Paule
LATHE, Richard
                                                                                                                                                                                                                                                                                                 repeat_region 439..5239
                                                                           repeat_region 457
                                                                                                                                        mat_peptide
121..5661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHARMACEUTICAL COMPOSITION FOR THE TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
  /note= "Nucleotide 457 is X1 = NNN
which is the codon for Pro or Ala v
or CCG; and Ala = GCT, GCC, GCA, o)
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  Pro or Ala wherein GCC, GCA, or GCG."
                         Pro = CCT,
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RESULT 3
US-08-232-463-14/c
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                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/08232463 Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                           SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                          APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1645
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                 COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                                                         STREET: 1800 Dia
CITY: Alexandria
               APPLICATION NUMBER: FILING DATE:
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LOCATION:
CLASSIFICATION:
                                                                                                                                                                                                         ADDRESSEE:
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45.4%;
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which is the codon for Pro or Ala wherein
or CCG; and Ala = GCT, GCC, GCA, or GCG."
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which is the codon for Thr or Asn wherein Thr = ACT,
or ACG; and Asn = AAT or AAC."
                           US/08/232,463
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                                                                                                                                                                                          Suite
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GENERAL INFORMATION:
APPLICANT: Horlick, Robert A.
APPLICANT: Damaj, Bassam B.
APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Ger
TITLE OF INVENTION: From Multiple Transfected Episomes
FILE REFERENCE: 0867,119903US1
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 36
SOFFWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
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US-09-130-114-2/c
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Best Local S
Matches 25
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TELEX: 899149
INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                 Sequence 2, Application Patent No. 5976807
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ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           942 gctcgagggctccaggaaggtggaggaaggaagccccgggggaccccgaccacgaggc 1001
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                                                                                                                                                                                                                                                                                                                                                                           RRRRRRRRRRRRRRRRRRRRRRRATCGCAAGCTCCGACCTGCAGCCAAGCTCGG
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; LENGTH: 1931
; TYPE: DNA
; ORGANISM: EBNA
US-09-130-114-2
                                                                                      ; MOLECULE TYPE: US-08-770-379-17
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: Sequence 17, Application US/08770379

: Patent No. 5849564
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                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 5234:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 35100 base pairs
TYPE: nucleic acid
      Query Match
Best Local Similarity
Matches 221; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Chang,
APPLICANT: Bohenzk:
APPLICANT: Russo,
APPLICANT: Edelman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.2
Best Local Similarity 63.8
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF TOTAL NUMBER OF THE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
ADDRESSEE: Cooper & Dunham LLP
AVenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1003 GTGACGGAGCTGGGGCCGGAGGTGGAGGACGAGGACGGGGAGGACGAGGACGGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York COUNTRY: U.S.A. ZIP: 10036
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Russo, James J.
Edelman, Isidore S.
Moore, Patrick S.
      Conservative
                                                                                                                  linear
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                                                                                                  DNA (genomic)
                                                                                                                                   double
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                   3.0%;
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 Score 70.2; DB 3; Pred. No. 8.9e-06; ); Mismatches 228;
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Pred. No. 6.4e-07;
0; Mismatches 64;
                                Length 35100;
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RESULT 6
US-09-050-863-2
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Patent No. 61141
                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-65
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Lao, Y
                                                           TELEFAX: (415) 949-8711
INFORMATION FOR SEQ ID NO:
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                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                    SOFTWARE: Patentin Rela
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hiang, Betty
APPLICANT: Payan, Don
TITLE OF INVENTION: Mammal:
TITLE OF INVENTION: System
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                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Flehr, Hohbach, Test, Albritton STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco
            STRANDEDNESS:
                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 94111-4187
                           TYPE:
                                      LENGTH:
 FOPOLOGY:
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unknown
            unknown
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US-09-050-863-2

DNA

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Query Match
Best Local Similarity
Watches 229; Conserv
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US-09-130-114-1/c
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APPLICANT: HOrlick, Robert A.
APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing
TITLE OF INVENTION: From Multiple Transfected Episomes
FILE REFERENCE: 0867/1D903USI
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEC ID NOS: 36
NUMBER OF SEC ID NOS: 36
                                                                                                                                                          SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 5452
TYPE: DNA
ORGANISM: VEBNA
S-09-130-114-1
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Best Local Similarity
Matches 229; Conserv
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ggacctgtgggccagagcatagcaagggtgg---gggcagggtggacgagggggccccagc
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                                     ggaaggtggaggaaggaagccccggggacccccgaccagggccagcacccagggtc 1015
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47.78;
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                                                                                         Score 67.2; DB 4;
Pred. No. 2.5e-05;
0; Mismatches 248;
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Pred. No. 2.1e-05;
                                                                                          248;
                                                                                                                   Length 5452;
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; TOPOLOGY: US-07-884-811-15
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US-07-884-811-15
Sequence 15, Application US/07884811
Patent No. 5316921
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                                                                                       TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION: APPLICANT: Godows
                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1918
                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 10596 bases
                                                                                                                                                           REFERENCE/DOCKET NUMBER: 75
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1738
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                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
                                                                                                                                                                                                                                                           CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 450 rounce CITY: South San Francisco STATE: California
                          LENGTH: 10596 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: UFILING DATE: 19920518
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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460 Point San Bruno
                                                                                                                              3: 415/225-3216
415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Godowski, Paul J. Lokker, Nathalie A. Mark, Melanie R. VENTION: SINGLE-CHAIN HEPATOCYTE GROWTH FACTOR VARIANTS
               linear
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Query Match Best Local Similarity

2.98;

Score 67.2; Pred. No. 2.

DB 1; .8e-05;

Length 10596;

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RESULT 9
US-07-885-971-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15, Application US/07885971 Patent No. 5328837
                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: GOOGWSKI, Paul J. 1
TITLE OF INVENTION: HEPATOCYTE
NUMBER OF SEQUENCES: 21
                          TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                APPLICATION NUMBER: US, FILING DATE: 19920518 CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION NUMBER:
SEQUENCE CHARACTERISTICS:
LENGTH: 10596 bases
                                                 REFERENCE/DOCKET NUMBER: 77
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2707
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                                                                                                                                                                                                                                                                                                                                     STATE: C
                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggacccaggaagtgggcggtcaggaccttggggaggcagtgcagcccagccccc
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TE GROWTH
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RESULT 10
US-08-087-783A-15
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                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb flo
COMPUTER: IBM PC compatable
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wildpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,783
FILING DATE: 13-Jul-1993
                                                                                                                                                                                                                                                                                                                                                            Sequence 15, Application US/08087783A
Patent No. 5547856
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Lok
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Best Local Similarity
       CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/884811
FILING DATE: 18-MAX-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/885971
                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NUMBER OF SEQUENCES:
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ZIP: 94080
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CITY: South San Francisco
STATE: California
FILING DATE:
                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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EDNESS: single
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18-MAY-92
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                                                                                                                                                                                                                                                                                                                                               Paul J., Lokker,
HEPATOCYTE GROWTH
                                                                                                                   US/08/087,783A
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Pred. No. 2.8e-05;
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ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L. REGISTRATION NUMBER: 35,600

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US-08-194-088B-15
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Best Local Similarity
Matches 229; Conserv
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
                                                                                                                                                          TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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TYPE: Nucleic Acid
STRANDEDNESS: Single
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47.78;
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Pred. No. 2.8e-05;
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FACTOR VARIANT
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RESULT 12
US-08-194-087-15
Sequence 15, Application US/08194087
Patent No. 5879910
GENERAL INFORMATION:
APPLICANT: GODOWSKI, Paul J. LOKK
TITLE OF INVENTION: HEPATOCYTE GRC
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Best Local Similarity 47.7%;
Matches 229; Conservative
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APPLICATION NUMBER: US/08/194,088B
FILING DATE: 09-FEB-1994
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FILING DATE: 18-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gallegos, R. Thomas
REGISTRATION NUMBER: 32,6
            CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    956 ggaaggtggaggaaggaagccccgggggaccccgaccacgaggccagcacccagggtc 1015
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STRANDEDNESS: single
ADDRESSEE:
STREET: 4
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TELEX: 910/371-7168
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Pred. No. 2.8e-05;
 Blvd
                                                          LOkker, Nathalie A. mark, Melanie R. E GROWTH FACTOR PROTEASE DOMAIN VARIANTS
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South San Francisco California

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RESULT 13
PCT-US93-04648-15
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Best Local Similarity 47.7%;
Matches 229; Conservative
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INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 10596 bases
TYPE: nucleic acid
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                                                                    2707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 18-MAY-1992 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Dreger, Ginger R. REGISTRATION NUMBER: 33,055 REFERENCE/DOCKET NUMBER: 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                    tgggagccagggtggccgacaaggtgaggaaggaggaaggtgggatggggg
                                                                                                                                   ggacccaggaagtgggcggtcaagaccctggggaggcagtgcagccctgcgccaacccc
                                                                                                                                                                                                                                                                                                                                                      cacggagcgtggagccccagggatgcgggacccctggagaggagccagggggatgaggcag 1132
                                                                                                                                                                                       tggagaagatcgctctgaatttggaggggtgtgccctcagccagggcagcctcaggacgg
                                                               tggagctgagccggcgggagcagccgccacagagccaggcctcagagtgcctcagagg
                                                                                                                                                                                                                                                                              9999ccac9999aagata99ccggagcccttaagccccaaagagagcaagaagaggaagc 1192
                                                                                                                                                                                                                                                                                                                                  ggacctgtgggccagagcatagcaagggtgg---gggcagggtggacgaggggccccagc 1072
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  PC/TUS9304648
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Pred. No. 2.8e-05;
0; Mismatches 248
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PCT-US93-04648-15
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 10596 bases
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 07/884
FILING DATE: 18-MAY-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/885
FILING DATE: 18-MAY-92
ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: 75
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04648
FILING DATE: :19930517
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Genentech, Inc., Godowski, Paul J., Lokker, TITLE OF INVENTION: HEPATOCYTE GROWTH FACTOR VARIANTS
                                                                                                                                                                                                                                                                                                                                         7 Match 2.9%;
Local Similarity 47.7%;
nes 229; Conservative
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
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99acccaggaagtgggcggtcaggaccctggggaggcagtgcagccctgccgccaacccc 1372
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2.8e-05;
les 248;
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US-07-945-283-1
                                                              ; LOCATION:
US-07-945-283-1
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/945,283 FILING DATE: 1920911 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                               TOPULOS. DNA MOLECULE TYPE: DNA HYPOTHETICAL: NO
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NFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 309-685-4011 ext.513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis P. Ribando
STREET: 1815 No. 5352596th University Street
                                                                                                              FEATURE:
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LENGTH: 8438 base pair
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NAME: Ribando, Curtis P
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                         FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
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LOCATION:
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replace(1566, "c")
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                                                                             replace(7010, "g")
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 2.6%;
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 Score 61.8; DB 1;
Pred. No. 0.00033;
                Length 8438;
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                                                                                                                  ; NAME/KEY:
; LOCATION:
US-08-728-323A-1
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US-08-728-323A-1
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                                     Query Match 2.9
Best Local Similarity 57.9
Matches 107; Conservative
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Sequence 1, Apra-
No. 5948676
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                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575
TELECOMMUNICATION INFORMATION:
TELECHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5596
                                                                                                                                                                                  STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA (gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5716 GTCGCTGCC 5724
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CITY: New York
STATE: New York
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2 agaattcagcggccgctgaattctagccgagcatggacgaccccgactgcgactccacct 61
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10036
                                                                                                                                                                                                                               nucleic acid
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1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                               212-391-0525
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Moore, Patrick S.
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                                                                                                                                                                                  DNA (genomic)
                                                    2.6%;
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                                   Score 60.2; DB 4;
Pred. No. 0.00059;
0; Mismatches 78;
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                                                                   Length 3489;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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SUMMARIES

Ouery Match Length DB I 98.1 1232 11 77.6 1676 11 77.6 2423 11 77.6 2483 11 77.4 2423 11 46.6 2208 12	th DB ID 12 11 AF172449 16 11 AF172450 11 AF172451 13 11 AF172453
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2 agon, I.S., Verderame, M.F., Allen, S.S. and Direct Submission
Submitted (26-JUL-1999) Department of Neuro Pennsylvania State University College of Me Drive, Hershey, PA 17033, USA Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1232)
Zagon, I.S., Verderame, M.F., Allen, S.S. and McLaughlin, P.J.
Cloning, Sequencing, Chromosomal location, and function of
encoding an opicid growth factor receptor (OGFr) in humans
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2 (bases
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Submitted (26-JUL-1999) Department of Pennsylvania State University College Drive, Hershey, PA 17033, USA
                                                                                                                                                                                                                                                           Zagon, I.S., Verderame, M.F., Allen, S.S. and McLaughlin, P.J. Cloning, sequencing, chromosomal location, and function of encoding an opioid growth factor receptor (OGFr) in humans in Res. 856 (1-2), 75-83 (2000)
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SKGGRVDEGPQPRSVEPQDAGPLERSQGDEAGGHGEDRPEPLSPKESKKRKLELSRR
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Homo sapiens opioid gu
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Zagon, I.S., Verderame, M.F., Allen, S.S. and McLaughlin, P.J. Cloning, sequencing, chromosomal location, and function of encoding an opioid growth factor receptor (OGFr) in humans parameters. 856 (1-2), 75-83 (2000)
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Zagon, I.S., Verderame, M.F.,
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/product-"opioid growth factor receptor"
/product-1d-"AAF64404.1"
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/db_xref="G17595303"
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QEIQERLVRAFELHAGFYGIRLEDNHSYYQWLFARVERONLWRTTRILK
SPCELSLEHFQAPLVRFFLEETLVRRELPGVRQSALDYFMFAVRCRHQRRQLVHFAWE
HFRPRCKFVWGFQDKLRFKFSSLJHPLLGSRKYVEEGSSFGDPDHEASTQGRTGCPEH
SKGGGRYUDEGDQPSFVEPDAGPLERSKRKYEEGSSFDDPHEASTQFVEFARR
EQPFTEPGPQSASEVEKIALNLEGCALSQGSLRTGTQEVGGQDFGEAVQFCQPLGAR
VADKVEKRRKVDEGAGDSAAVASGGAQTIALAGSPAFSGHFKAGHSENGVEEDTEGRT
GPKEGTPGSPSETPGFSPAGPAGDEPAESPSETPGPRFAGPAGDEPAESPSETPGFP
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Ivania State University College
Hershey, PA 17033, USA
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/db_xref="taxon:9606"
/chcmosome="20"
/map="20q13.3"
/tissue_type="placenta"
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Primates;
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Craniata; Vertebrata;
Catarrhini; Hominidae
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Zagon, I.S., Verderame, M.F.,
Direct Submission
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Zagon, I.S., Ver
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SEEPRAARPSSFQSKWTGSRNWRATRDWCRYRHMYPDLVERDCNODTPNLSFYRNEIR
FLPNGCFIEDILQNWTDNYDLLEDNHS; IQMLFPLREGVNWHAKPLTLREVPKSS
QEIQERLVRAYELMLGFYGIRLEDNHS; IQMLFPLREGVNWHAKPLTLREVPKSS
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SKGGGRVDEGPOPRSVEPQDAGPLERSQGDEAGGHGEDRPEPLSFRESKKKRLELSGR
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/chromosome="20"
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Zagon, I.S., Verderame, M.F., Allen, S.S. and McLaughlin, P.J. cloning, sequencing, chromosomal location, and function of encoding an opioid growth factor receptor (OGFr) in humans Brain Res. 856 (1-2), 75-83 (2000)
                                                                                     Pennsylvania State University Drive, Hershey, PA 17033, USA Location/Qualifiers
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Zagon, I.S., Verderam
Direct Submission
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AF109134.1 G
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1 (bases 1 to 2423)

Liu, J., Brewton, R.G., Takanosu, M., Wood, B.M. and Mayne, R.

Cloning of 7-60: A human gene from chromosome 20q13.3 which encode a novel intracellular protein motif repeated seven times
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (23-NOV-1998) Cell Biology, University of Alabama at Birmingham, 1670 University Blvd. VH302, Room 605, Birmingham, 35294, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu, J., Brewton, R.G., Takanosu, M., Direct Submission
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Query Match

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DB 11;

Length 2423;

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RESULT

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CONSETVALIVE 0; MISMATCHES acgaggaggatgcggaggacgcgaggacgaggacgagacgacgacgacgac	1 1549. 1764 1 1549. 1764 /note="imperfect" /rpt_type=direct /rpt_unit=15491575 20312036 2203 22 a 615 c 675 g 396 t 22 a 615 c 675 g 396 t 22 a 615 c 675 g 396 t 23 a 615 c 675 g 396 t 24 a 615 c 675 g 396 t 25 a 615 c 675 g 396 t 26 a 615 c 675 g 396 t 27 a 615 c 675 g 396 t 28 a 615 c 675 g 396 t	/note="[met-5]-enkephalin binding protein" /codon_start=1 /product="opioid growth factor receptor" /product="opioid growth factor receptor" /protein_id="AAF25002.1" /protein_id="AAF25002.1" /db_xref="G1:6693832" /taanslation="wbopcobsTweeeseegeegedgedgedgedgedgedgedgedgedgedgedge	orvegicus" "l6" "old fetus"	E 20074706 E 2 (bases 1 to 2208) E 2 (bases 1 to 2208) S Zagon, I.S., Verderame, M.F., Allen, S.S. and McLaughlin, P.J. S Direct Submission L Submitted (04-JUN-1999) Neuroscience and Anatomy, Penn State University College of Medicine, 500 University Drive, Hershey, PA 17033, USA	Rattus. 1 (bases 1 to 2208) 1 (bases 1 to 2208) 2agon,I.S., Verderame,M.F., Allen,S.S. and McLaughlin,P.J. 2agon, Sequencing, expression and function of a cDNA encoding a receptor for the opioid growth factor, [Met(5)]enkephalin Brain Res. 849 (1-2), 147-154 (1999)	AF156878 2208 bp mRNA ROD 16-JAN-2000 Rattus norvegicus opioid growth factor receptor mRNA, complete cds. AF156878.1 G1:6693831 Norvey rat. Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;

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Submitted (09-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: hunquery@sanger.ac.uk clone requestes: clonerequest@sanger.ac.uk
On Jul 8, 2000 this sequence version replaced g1:8919619.
During sequence assembly data is compared from overlapping clon
                                                                                                                                                                                             Human DNA sequence from 20q13.2-13.33, complete AL035669
                                                                                     Smith, M.
                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 160241)
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Em., EMBL; Swr. SWISSPROT; TT: TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the sanger Centre Chromosome 20 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr20
RP5-885L7 is from the library RPCI-5 constructed at the Roswell RPark Cancer Institute by the group of Pieter de Jong. For further underlis see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is the entire insert of clone RP5-885L7 The true left end of clone RP4-563E14 is at 140192 in this sequence. The true right end of clone RP11-93B14 is at 44512 in this sequence.
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/note="12 copies 80 mer 61% conserved"

complement(4223. .5153)

/note="Tandem repeat: region contains two forced joins single clone. Assembly consistent with restriction
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/clone="RP5-885L7"
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/db_xref="taxon:9606"
/chromosome="20"
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mer

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4 copies 48 m

2017. 18496

/note="3 cor'

18319.
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18319. 18486
/note="7 co-18320
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/note="18 copies 31 mer 71% conserved"

4533. .4822

/note="5 copies so
/note="7 copies 24 m
18320. .18495
/note="44 copies 4 m
18321. .18496
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/note="44 copies 6 n
16664. .16885
/note="3 copies 74 n
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4720. .5137
/note="11 copies 38
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/note="13 copies 4 mer gaag 100% conserved"
17287. .17411
/note="MER5A repeat: matches 35. .165 of consensus"
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/note="10 copies 4
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7892. .8074
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7224. .7451
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5051. .5164
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te-"16 copies 16
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1 Homo sapiens 7-60 g

AF112980

AF112980.1 GI:41300
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32; Conservative
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20722. .20806
/note="5 copies 17 m
21349. .21410
/note="2 copies 31 me
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18325. .18486
/note="9 copies 18 me
18327. .18486
/note="8 copies 20 me
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20704. 20805
/note="3 copies 34 n
20710. 20811
/note="2 copies 51 n
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19839..19954
/note="2 copies 58 n
20020...20103
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/note="Alu repeat: matches 238.
24787. .24847
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21584. .21654
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/note="MLT1D repeat:
25853. .26065
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Pred. No. 4.3e-43;
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Submitted (10-DEC-1998) Cell Biology, University of Alabama ;
Birmingham, VH 302, Room 605, Birmingham, Alabama 35294, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 6670)

Takanosu,M., Liu,J. and Mayne,R.
Genomic Structure of Human Gene 7-60
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete sequence of the 23-kilobase human COL9A3 gene. Detection of Gly-X-Y triplet deletions that represent neutral variants J. Biol. Chem. 274 (32), 22469-22475 (1999)
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10536. .10592
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16335. 1638
16491. 16562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Whitton, J.L., Rixon, F.J., Easton, A.J. and Clements, J.B. Immediate-early mRNA-2 of herpes simplex viruses types 1 and 2 unspliced; conserved sequences around the 5' and 3' termini correspond to transcription regulatory signals Nucleic Acids Res. 11 (18), 6271-6287 (1983)
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Nucleotide sequences of the joint between herpes simplex virus types 1 and 2

J. Gen. Virol. 55 (Pt 2), 315-331 (1981)
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Alphaherpesvirinae; Simplexvirus.
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2496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic DNA for 0.74-0.84 region,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         membrane glycoprotein"
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                                                                                                                                                                                                                                                                     polyA_signal
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                                                                                                                                                                                                                                                                                                                                                                 /number=]
                                                                                                                                                                                                                                                                                                                                                                                                                                  /number=2
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/product="Vmw118(ICP0)"
complement(11474. .11478)
/note="for RL2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="start of internal large repeat" 6594. .8808
                     /translation="MSRRRGPRRRGPRRRPRPGAPAVPRPGAPAVPRPGALPTADSQM
VPAYDSGTAVESAPAASSLLRRWLLVPQADDSDDADYAGNDDAEWANSPPSEGGGKAP
EAPHAAPAAACPPPPPRKERGPQRPLPPHLALRLRTTTEYLARLSLRRRRPPASPPAD
                                                                                                                                                                                                                                                           complement(11876. .11881)
/note="for RL1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAPAWSRRTLLPEHARNCVRPPDYPTPPASEWNSLWMTPVGNMLFDQGTLVGALDFH
GLRSRHPWSREQGAPAPAGDAPAGHGE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="UL56 ORF"
/protein_id="BAA01271.1"
/protein_id="BAA01271.1"
/db_xref="G1:221790"
/translation="MALGAGHAHACRDDGDDSVIDAPPPYESVAGASAGQFVVIDIDT
/translation="MALGAGHAHACRDDGDDSVIDAPPPYESVAGASAGQFVVIDIDT
PTDSPPYSAGTSPVCLVSPASSGDGEVCERGRSRRAAWRAARRRAERRAFRRSF
GPGGLFVETPLFLPETMIGAHPGVGGDLPSGLPTYAEATSDRPPTYAMVMAACPTEPP
GGSVUGPADQPRVQSSRTWRPPLVNSRELYRAQRAARCASSSDTPQAPGWCGGTCRHAV
                                                                                                /product="neurovirulence
/protein_id="BAA23428.1"
/db_xref="GI:2626943"
                                                                                                                                                                                                        complement(join(12240. .12530,12685. .13179))
/note="RL1 ORF"
                                                                                                                                                                                                                                                                                                                                                                                                              complement(<11242.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(10156. .10834)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(<8251. .9974)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDSEEETEVGISDDDLHRDSTSEAGSTDTEMFEAGLMDAATPPARPPAERQGSPTPAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(8251. .9974,10156. .10834,11242. .11316))
/note="RL2 ORF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(7996. .8001)
/note="for RL2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="right extremity of long unique region" 4356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(3413. .3418)
/note="for UL56"
complement(3444. .4151)
<sup>a</sup>prgkvcfsprvqvrhlvawetaarlarrgswareradrdrfrrrvaaaeavigpcle
                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="Vmw118(ICP0)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product-"Vmw118(ICPO)"
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/protein_id="BAA23427.1"
/db_xref="G1:3626942"
/translation="MEPRPGTSSRADPGPERPPRQTPGTQPAAPHAWGMLNDMQWLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6594. .8808
/note="latency associated transcript (pot.)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FGVVAVVVVIILAFLWR"
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/note="for UL55"
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Laarsylvrascs:sgpihcfffavkdsqhslplytelrnfadlynhppylreledk
RGGELRCTGPFSCGTIKDVSGASPAQEXTINGIVYHCHCRYPFSKTCWLGASAALQHL
RSISSSGTAARAAEQRRHKIKIKIKV"
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/db_xref="GI:221789"
                                                                                                                                                                                                                                                                                                                                                                                                                   .11316)
                                                                                                                                                   factor(ICP34.5)"
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HSV2HG52
LOCUS
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ORGANISM
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                   genome; deoxyribonuclease; deoxyuridane triphosphatase; DNA
polymerase; envelope protein; glycoprotein B; glycoprotein C;
glycoprotein D; glycoprotein B; glycoprotein G;
glycoprotein I; glycoprotein J; glycoprotein K; glycoprotein I;
glycoprotein I; glycoprotein J; glycoprotein K; glycoprotein I;
glycoprotein M; host shut-off factor; integral membrane protein;
major capsid protein; membrane-associated phosphoprotein kinase;
ribonucleotide reductase large subunit; ribonucleotide reductase
small subunit; RL1 gene; RL2 gene; RS1 gene; tegument protein;
thymidine kinase; UL1 gene; UL10 gene; UL17 gene; UL12 gene; UL13
gene; UL14 gene; UL15 gene; UL12 gene; UL12 gene; UL19
gene; UL12 gene; UL16 gene; UL12 gene; UL12 gene; UL19
gene; UL13 gene; UL30 gene; UL31 gene; UL32 gene; UL39
gene; UL3 gene; UL30 gene; UL31 gene; UL32 gene; UL39
gene; UL40 gene; UL36 gene; UL37 gene; UL39 gene; UL49
gene; UL40 gene; UL41 gene; UL43 gene; UL44 gene; UL49
gene; UL40 gene; UL41 gene; UL43 gene; UL44 gene; UL50
gene; UL50 gene; UL51 gene; UL52 gene; UL50
gene; UL50 gene; UL51 gene; UL52 gene; UL50
gene; UL50 gene; UL51 gene; UL51 gene; UL50
gene; UL50 gene; UL51 gene; UL50 gene; UL50
gene; UL50 gene; UL50 gene; 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ggacgaggagtcggaggaggccgcgggcgcggcccag 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ggacgaggactgcgaggacgccgccggcgcgagggacgcggggacgcaggggacga 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gacgaccccgactgncgactccacctgggaggaggacgaggaggaggatgcgggaggacgcggga 96
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0.74-0.84 genome % units.
                                                   McGeoch,D.J., Moss,H.W., McNab,D. and Frame,M.C.
DNA sequence and genetic content of the HindIII 1 region i short unique component of the herpes simplex virus type 2 identification of the gene encoding glycoprotein G, and
                                                                                                                                                      Alphaherpesvirinae; Simplexvirus.

1 (bases 1 to 154746)

MCGeoch D 7 ...
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capsid associated tegument protein; capsid protein; complete
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                            lutionary comparisons
                                                                                                                                                                                                                                      herpesvirus 2
es; dsDNA viruses,
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                                                                                                                                                                                                                                                                            herpesvirus 2. herpesvirus 2
                                                                                                                                                                                                                                                                                                                            US9 gene
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5124 c 4789 g 1893 t
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complement(13338. .13341)
/note-"for RL1"
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complement(12685. .>13179)
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13619
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pe 2 (strain HG52), complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 (bases 1 to 154746)
Barnett, B.C., Dolan, A., Telford, E.A., Davison, A.J. and McGeoch, D.J. A novel herpes simplex virus gene (UL49A) encodes a putative membrane protein with counterparts in other herpesviruses J. Gen. Virol. 73 (Pt 8), 2167-2171 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 (bases 1 to 154746)
McGeoch,D.J., Cunningham,C., McIntyre,G. and Dolan,A.
McGeoch,D.J., Cunningham,C., McIntyre,G. and Dolan,A.
Comparative sequence analysis of the long repeat regial adjoining parts of the long unique regions in the gen simplex viruses types 1 and 2
J. Gen. Virol. 72 (Pt 12), 3057-3075 (1991)
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Everett,R.D. and Fenwick,M.L.
Comparative DNA sequence analysis of the ho
different strains of herpes simplex virus:
encodes a truncated UL41 product
J. Gen. Virol. 71 (Pt 6), 1387-1390 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (08-DEC-1999) A. Dolan, MRC Street, Glasgow, Gll 5JR, UK On Dec 13, 1999 this sequence version Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dolan, A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Street,, Glascrevised bu [6]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (25-FEB-1997) A. Dolan, Street,, Glasgow,, Gll 5JR, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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2303. .2377
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943. .1070
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461. .547
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255
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1738. .1743
2303. .5368
                                                                                                                                                              /rpt_family="5"
1089. .1379
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/db_xref="GI:1869821"
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//cene="RL1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         440. .1379
/gene="RL1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="human herpesvirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="start of TRL (terminal copy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10310"
                                                                                                                         'number=2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
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ex virus: type 2 strain HG52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             replaced gi:1869820
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e genomes of herpes
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10211. 10078
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VGRRDLRPANTTSTWEPPVSSDDEASSQSKPLATQPPVLALSNAPPRRVSPTRGRRRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="UL1"
9427. .1010:
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9427. .10101
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9276. .9297
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/gene="RL2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="virion glycoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="proposed LAT splice donor site (5'
LAT species)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(7025)
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/gene="RL2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLRSRHPWSREQGAPAPAGDAPAGHGE"
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/db_xref="SWISS-PROT:P28284"
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DEFINITION
ACCESSION
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KEYWORDS
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ORGANISM
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TITLE
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Best Local Simi
Matches 101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97
                                                                                                                                                                                                                                                                                              capsid associated tegument protein; capsid protein; complete genome; deoxyribonuclease; deoxyruidine triphosphatase; DNA polymerase; envelope protein; glycoprotein B; glycoprotein C; glycoprotein D; glycoprotein B; glycoprotein G; glycoprotein H; glycoprotein B; glycoprotein H; glycoprotein B; glycoprotein H; glycoprotein M; host shut-off factor; integral membrane protein; major capsid protein; membrane-associated phosphoprotein kinase; ribonucleotide reductase large subunit; ribonucleotide reductase small subunit; RL1 gene; RL2 gene; RS1 gene; tegument protein; thymidine kinase; U115 gene; U116 gene; U117 gene; U118 gene; U119 gene; U120 gene; U120 gene; U130 gene; U140 gene; U150 ge
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McGeoch,D.J., Moss,H.W., McNab,D. and Frame,M.C.
DNA sequence and genetic content of the HindIII 1 region in the short unique component of the herpes simplex virus type 2 genome: identification of the gene encoding glycoprotein G, and
                                                                                                      Viruses; dSDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Simplexvirus.

1 (bases 1 to 154746)
McGeoch, D. J., Moss, H.W., McNab, D. and Frame, M.C.
                                                                                                                                                                                                                                           human herpesvirus 2.
human herpesvirus 2
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simplex virus
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SIDELGRRQLTDTIRKDLRLSLAKFSIACTKTSSFSGTAARQRKRGAPPQRTCYPRSN
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/db_xref="GI:1869825"
/db_xref="SPTREMBL:Q89644"
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11033. .1173
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LTVKRGAAASHSKLGWDRFVGGVVQRLAARRPGLVFMLWGAHAQNAIRPDPRQHYVLK
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63.5%;
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92356101
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McGeoch,D.J., Cunningham,C., McIntyre,G. and Dolan,A.
Comparative sequence analysis of the long repeat regions and
adjoining parts of the long unique regions in the genomes of herpes
simplex viruses types 1 and 2
J. Gen. Virol. 72 (Pt 12), 3057-3075 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 154746)
Everett,R.D. and Fenwick,M.L.
Comparative DNA sequence analysis of the host shutoff genes of different strains of herpes simplex virus: type 2 strain HG52 encodes a truncated UL41 product
J. Gen. Virol. 71 (Pt 6), 1387-1390 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (08-DEC-1999) A. Dolan, MRC Virology Unit, Church Street, Glasgow, Gl1 5JR, UK
On Dec 13, 1999 this sequence version replaced gi:1869820.
Location/Qualifiers
1. .154746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (25-FEB-1997) A. Dolan, Street, Glasgow, G11 5JR, UK revised bu [6] 6 (bases 1 to 154746)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barnett, B.C., Dolan, A., Telford, E.A., Davison, A.J. and McGeoch, D. A novel herpes simplex virus gene (UL49A) encodes a putative membrane protein with counterparts in other herpesviruses J. Gen. Virol. 73 (Pt 8), 2167-2171 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dolan, A.
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                                                                                                                                                                 1089. .1379
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                                                                                                                                                                                                                                                            /rpt_family="6"
943. .1070
                                                                                                                                                                                                                                                                                                                    /rpt_family="7"
461. .547
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1738. .1743
2303. .5368
                                                                                                                                                                                                                                                                                                                                                                                                      PEARARARARAHEDGGPAEEEEAAAAARGSSAAAGPGRRAV"
                                                                                                                                                                                                                                                                                                                                                                                                                                 EAPHAAPAAACPPPPPRKERGPQRPLPPHLALRLRTTTEYLARLSLRRRRPPASPPAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="mSrrrgprrrgprrrppgapavprpgapavprpgateTaDSQM/translation="mSrrrgprrkgprrrppgapavprpgateTaDSQM/translation="mSrrrgprrkgprrkppgapavprpgapavprpgateTaDSQM/translation="mSrrrgprrkgprrkppgapavprpgapavprpgateTaDSQM/translation="mSrrrgprrkgprrkgprapavprpgapavprpgateTaDSQM/translation="mSrrrgprrkgprrkgprapavprpgapavprpgateTaDSQM/translation="mSrrrgprrkgprrkgprapavprpgapavprpgapavprpgateTaDSQM/translation="mSrrrgprrkgprrkgprapavprpgapavprpgapavprpgateTaDSQM/translation="mSrrrgprrkgprrkgprapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavprpgapavpr
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1089. .1379
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                                                                                                                                                  /number=2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="start of TRL (terminal copy of Long Repeat region)"
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                                                                                                                                                                             /gene="UL2"
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9427. .10101
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9427. .10101
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                                                                                                                                    10211. .10978
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9298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAPAWSRRTLLPEHARNCVRPDDYPTDPASEWNSLWMTPVGNMLFDQGTLVGALDFH
GLRSRHPWSREQGAPAPAGDAPAGHGE"
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/gene="RL2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="proposed LAT splice donor site (5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'rpt_family="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /number=2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       function="modulator of cell state and gene expression"
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ggaggaggacgaggatgcggaggacgcggaggacgaggactgcgaggacggcgaggc 123
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                                                                                                                                                                                                                                                                                                       Armour,J.A., Neumann,R., Gobert,S. and Jeffreys,A.J.
Isolation of human simple repeat loci by hybridization selection
Hum. Mol. Genet. 3 (4), 599-565 (1994)
                                                                                                                                                                                                                                                                                                                                                           Submitted (06-DEC-1993) J.A.L. Armour, Dept. of Genetics, University of Leicester, University Road, Leicester LEI 7RH, 2 (bases 1 to 236)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H.sapiens DNA
X76589
                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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/db_xref="taxon:9606"
/clone="wg2c3"
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/translation="MYKSRVSYRSVMSGVGEERVPSAFTILASWGWTFAPQNHDPGAS
/translation="MYKSRVSYRSVMSGVGEERVPSAFTILASWGWTFAPQNHDPGAS
PNTTPIESIAGTAPDAHVGPLDGEPDRDAISPLTSSVAGDPPGADGPYVTFDTLFMVS
SIDELGRRQLTDTIRKDLRLSLAKFSIACTKTSSPSGTAARQRKRGAPPQRTCVPRSN
KSLQMFVLCKRANAAQVREQLRAVIRSRKPKYYTRSSDGRLCPAVPVFVHEFVSSEP
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HPGQAHGLAFSVRADVPVPPSLRNVLAAVKNCYPDARMSGRGCLEKWARDGVLLLNTT
LTVKRGAAASHSKLGWDRFVGGVVQRLAARRPGLVFM.WGAHAQNAIRPDPRQHYVLK
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/gene-"UL3"
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Birren,B., Linton,L., Nusbaum,C
Mus musculus, clone RP23-178A24
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Unpublished
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Rodentia;
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1081 1180: gap 1181 3071:

1080:

2 3171: gap (2 4943: qap (

3: gap (

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NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Quality coverage: 4.8 in Q20 bases; agarose-fp
Quality coverage: 4.8 in Q20 bases; sum-of-contigs
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840 13939: gap of
940 17082: contig of 3143 bp in length
1083 17182: gap of
100 bp
1183 20437: contig of 3255 bp in length
138 24737: contig of 3255 bp in length
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151 32961: contig of 3577 bp in length
152 28514: gap of
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153 32961: contig of 4447 bp in length
156 40185: gap of
167 4047 bp in length
168 40185: gap of
168 40185: gap of
168 40185: gap of
168 40185: gap of
169 54164: gap of
169 54164: gap of
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165 54164: gap of
167 309 bp in length
168 63467: gap of
169 54164: gap 
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38 8188: contig of 100

89 8288: gap of 10317: contig of 2

189 10317: gap of 11
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/db_xref="taxon:10090"
/clone="RP23-178A24"
    'clone_lib="RPCI-23 Female Mouse BAC"
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126702: contig of 11470 k
26802: gap of 100 bp
139890: contig of 13088 b
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214721: cont
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153374: cont
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15132: contig of 11119 bp in length
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82165: contig of 13871 l
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1 (bases 1 to 1676)

Zagon, I.S., Verderame, M.F., Allen, S.S. and McLaughlin, P.J.

Cloning, Sequencing, Chromosomal Location, and function of cDNAs encoding an opioid growth factor receptor (OGFr) in humans Brain Res. 856 (1-2), 75-83 (2000)
                                                                                  Pennsylvania State University College
Drive, Hershey, PA 17033, USA
Location/Qualifiers
                                                                                                        Zagon, I.S., Verderame, M.F., Allen, S.S. Direct Submission Submitted (26-JUL-1999) Department of
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'product="opioid growth
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Zagon, I.S., Verderame, M.F., Allen, S.S. and McLaughlir Cloning, sequencing, chromosomal location, and functiencoding an opioid growth factor receptor (OGFr) in Brain Res. 856 (1-2), 75-83 (2000)
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Zagon; I.S., Verderame, M.F., Allen, S.S. and
Cloning, sequencing, chromosomal location,
encoding an opioid growth factor receptor (
Brain Res. 856 (1-2), 75-83 (2000)
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Drive, Hershey, PA 17033, USA
Location/Qualifiers
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Query Match 84.5 Best Local Similarity 98.6 Matches 1363; Conservative tagaattcagcggccgctgaattctagccgagcatggacgaccccgactgcgactccacc attgaggacattcttcagaactggacggacaactatgacctccttgaggacaatcactcc GACACGCCAAACCTGAGTTTCTACAGAAATGAGATCCGCTTCCTGCCCCAACGGCTGTTTC gacacgccaaacctgagtttctacagaaatgagatccgcttcctgcccaacggctgtttc agggacatgtgtaggtatcggcacaactatccggatctggtggaacgagactgcaatggg GCGGCGCGCCCAGCTCGTTCCAGTCCAGAATGACAGGGTCCAGAAACTGGCGAGCCACG 9cggcgcggcccagctcgttccagtccagaatgacagggtccagaaactggcgagccacg TGGGAGGAGGACGAGGATGCGGAGGACGCGGAGGACGACGACGACGACGACGACGAG tgggaggaggacgaggatgaggatgcggaggacgcggaggacgaggactgcgaggacggcgag AGGGACATGTGTAGGTATCGGCACAACTATCCGGATCTGGTGGAACGAGACTGCAATGGG 84.5%; 98.6%; Score 1352.2; DB 11; Pred. No. 1.1e-191; 1; Mismatches 19; Indels Length 2363; 0; Gaps 180 420 360 360 300 30C 240 240 180 120 120 60 60 0;

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Zagon, I.S., Verderame, M.F., Allen, S.S. and McLaughlin, P.J. Cloning, Sequencing, Chromosomal location, and function of encoding an opioid growth factor receptor (OGFr) in humans Brain, Res. 856 (1-2), 75-83 (2000)
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SPCELSIEHFQAPLVRRFFLEFILVRRELFGVRGSALDYEWFAVRCRHQRRQLVHFAWE
HFRPRCKFVWGPDGKLKRFKPSSLPHPLLGGSRKVEEBGSFGDPDHEASTGGRTCEPEH
SKGGGRVDEGPOPRSVEPDDAGPLERSQGDEAGGHGEDRPEPLSPKESKKRLELSRR
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ROPAGPAGDEPAESPSETPGPRAGPAGDEPAKIPSETPGPSPAGPTRDEPAESPSETPGP
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/map="20q13.3"
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/db_xref="taxon:9606"
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                               AGGGGACGAGGAGGAGTCGGAGGAGCCGCGGG-GGCCGTGCCCAGCTCGTTCCAGTC
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Liu,J., Brewton,R.G., Takanosu
Direct Submission
Submitted (23-NOV-1998) Cell B
Birmingham, 1670 University Bl
35294, USA
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Cloning of 7-60: A human gene from
a novel intracellular protein motif
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/PICHUCE / POW
/PICHELL_id="AAD03737.1"
/db_xref="GI:4139228"
/translation="MIGSRINWRATERDKCRYRHNYPDLYERDCNGDTPNLSEYRNEIRF
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LGELGLEHFQAPLYRFFLEESLYRRELPGVRQSALDYFMFAVGCRHQRRQLYHFAWEH
FRECKKYWGPODKLRREKPSSLPHPLEGSRKVEEEGSSPOEDPHEASTGGRTGCPEHS
KGGGRYUDEGPOPRSYDEPDAGFLERSQGDEAGGHGEDRPEPLSFKESKKRKLELSRRE
QPTIEPGPQSASEYEKIALNLEGCALSQGSLRTGTQEVGGQDPGBAVQPCRQPLGARV
ADKYRKRKVDEGAGDSAAVASGGAQTLALAGSPAPSGHFKAGHSENGYEEDTEGRTG
PKEGTPGSPSETPGPSPAGPTRDEFAESPSETPGPRPAGPAGDEPAESPSETPGFRPA
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/map="20q13.3"
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Blvd. VH302, Room 605
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Zagon, I.S., Verderame, M.F., Allen, S.S. and McLaughlin, P.J.
Clonling, sequencing, chromosomal location, and function of
encoding an opioid growth factor receptor (OGFr) in humans
Brain Res. 856 (1-2), 75-83 (2000)
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On Jul 8, 2000 this sequence version replaced gi:8919619.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; TT: TREMEL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of backerial clone contigs of human chromosome 20 constructed by the Sanger Centre Chromosome 20 monstructed by the Sanger Centre Chromosome 20 mapping Group. Further information can be found at http://www.sanger.ac.uk/MGP/Chr20
RP5-885L7 is from the library RPCI-5 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further Getails see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence is the entire insert of clone RP5-885L7 The true end of clone RP4-563E14 is at 140192 in this sequence. The true right end of clone RP11-93B14 is at 44512 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (09-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VECTOR: PCYPAC:
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                                                                                                                     __a6. .5152
/note="17 cc-
4308.
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4231. 5166
/note="234 copies 4 mer t
4240. 5151
/note="19 copies 48 mer 6
4248. 5159
/note="38 copies 24 mer 6
4264. 5163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /chromosome="20"
/map="q13.2-13.33"
/clone="RP5-885L7"
/clone_1ib="RPCI-5"
2.64
                             /note="14348..5
                                                                             4317. .5156
/note="21 co
/note="42 copies 4431. .5144
                                                                                                                                                                                                                                                                                                                                                                  /note="12 copies 80 mer 61% conserved" complement (4223. .5153) /note="Tandem repeat, region contains two single clone. Assembly consistent with res
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluJo repeat: matches 354..397 /note="L1MA9 repeat: matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="LIMA9 repeat: matches 6210. .6254 of consensus" 65. .353
                                                                                                                                                                                                                                                                                                                                                      single clone.
digest."
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/db_xref="taxon:9606"
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                               ="17 copies
.5145
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16582. .16891

/note="10 copies 31 mer 66% conserved"
16583. .16879

/note="9 copies 33 mer 66% conserved"
16585. .16840

/note="16 copies 16 mer 66% conserved"
16586. .16875

/note="15 copies 58 mer 72% conserved"
                                                                                                                      /note="5 copies 47 mer /
16848. 16899
/note="13 copies 4 mer 9
17287. 17411
                                                                                                                                                   /note="5 conf-
16848
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16500
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4456. .5148
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="11 copies 24 mer 68% conserved"
                                                                  17447. .17486
/note="10 copies 4 mer
18303. .18502
                                                                                                                                                                                          /note="44 copies 6
16664. 16885
/note="3 copies 74
                                                                                                                                                                                                                                                                         /note="7 copies 40 mer 67% conserved"
16598. .16837
/note="5 copies 48 mer 73% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11974. .12025

'Note="13 copies 4 mer ctca 73% conserved"

14394. .14478

'Note="5 copies 17 mer 77% conserved"
               18317.
                                                      note="5
                                                                                                            note="MER5A repeat:
                                                                                                                                                                                                                                                                                                                              16590. .16874
mote="15 copies 19 mer 64% conserved"
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note="17 copies 17 mer 65% conserved"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="6 copies 38 mer 98% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="L1M4 repeat: matches 4509. .5488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note-"19 copies 6
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4533. .4822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="MIR repeat: matches 86.
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              "4 copies 48
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ccgctgcaagttcgtctgggggccccaagacaagctgcggaggttcaagcccagctctct
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                                                                                                                                                                                                                     GCTGGTGCGGCGGGAGCTGCCGGGGGTGCGGCAGAGTGCCCTGGACTACTTCATGTTCGC
                                                                                                                                                                                                                                   gctggtgcggcgggagctgccgggggtgcggccagagtgccctggactacttcatgttcgc
                                                                                                                                                                CGTGCGCTGCCGACACCAGCGCCCCCCAGCTGGTGCACTTCGCCTGGGAGCACTTCCGGCC
                                                      CCGCTGCAAGTTCGTCTGGGGGCCCCCAAGACAAGCTGCGGAGGTTCAAGCCCAGCTCTCT
                                                                                                                                                                                                                                                                                                                                                                                 43.7%;
milarity 95.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="LTR16A repeat: 21779. .21852
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/note-"2 copies 51 mer 90% conserved"

20722. .20806

/note-"5 copies 17 mer 89% conserved"

21349. .21410

/note-"2 copies 31 mer 93% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18320. .18495

/note="44 copies 4 mer acac

18321. .18496

/note="11 copies 16 mer 64%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Alu repeat: matches 238. .311 of consensus" 24787. .24847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="4 copies 20 mer 76% 19839. .19954
                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MLTID repeat: matches 107.
25853. .26065
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/note="2 copies 74 mer 81%
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/note="9 copies 18 mer 66%
18327. .18486
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/note="7 copi
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19329. .19433
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1 (bases 1 to 2208)
2 agon, I.S., Verderame, M.F., Allen, S.S. and McLaughlin, P.J.
CLoning, sequencing, expression and function of a cDNA encoding receptor for the optoid growth factor, [Met(5)]enkephalin Brain Res. 849 (1-2), 147-154 (1999)
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Direct Submission
Submitted (04-JUN-1999) Neuroscience ar
University College of Medicine, 500 University
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Homo sapiens
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Direct Submission
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Takanosu, M., Liu, J.
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LGELGLEHFQAPLYRFFLEESLVRRELPGVRQSALDYFWFAVGCROROLYHFAWEH
FRPRCKFVWGPQDKLRFKFSSLPHPLEGSRKVEEEGSPGDPDHEASTQGTTGPEHS
KGGGRVDEGPOPRSVEPQDAGPLERSQGDEAGGHGEDRPEPLSPKESKKKLELSRRE
QPPTEPGPQSASEVEKIALNLEGCALSQGSLRTGTQEVGGQDPGEAVQPCRQPLGARV
                                                                                                                                                                                   join(<206.
4891. .>63
                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="20"
/map="20q13.3"
                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                         Eutheria;
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Primates;
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GCAGCCCTGCCGCCAACCCCTGGGAGCCAGG
                     ctgtccctgctgcaggggctggggcctccgg
                                                                                                                                                 CCCTCAGAGTGCCTCAGAGGTGGAGAAGATCGCTCTGAATTTGGAGGGGGTGTGCCCTCAG
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PKEGTPGSPSETFGPSPAGPAGDEPAESPSETPGPRPAGPAGDEPAESPSETPGPRPA
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                                                                   Armour, Direct Submission
Direct Submission
Submitted (06-DEC-1993) J.A.L. Armour, Dept. of Genetics,
University of Leicester, University Road, Leicester LE1 7RH, UK
2 (bases 1 to 236)
Armour, J.A., Neumann, R., Gobert, S. and Jeffreys, A.J.
Isolation of human simple repeat loci by hybridization selection
Hum. Mol. Genet. 3 (4), 599-565 (1994)
                                                                                                                                                                                                            Primates; Catarrhini; Hominidae;
1 (bases 1 to 236)
                                                                                                                                                                                                                                                                                             H.sapiens DNA 3' fl
X76589
X76589.1 GI:435154
                                                                                                                                                                                               Armour, J.A.L.
                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Vertebrata;
                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                simple repetitive
                                                                                                                                                                                                                                                                                                                                         HSRWG2C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997,
Location/Qualifiers
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Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.
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23; Conservative 240;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="wg2c3"
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                            Center: Whitehead Institute/ MIT Center code: WIBR
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NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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100 bp

58 63467: gap of 100 bp

58 73091: contig of 9624 b

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92 73191: gap of 100 bp

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20537: gap of 100 bp
24737: contig of 4200 bp in length
24837: gap of 100 bp
24837: gap of 3577 bp in length
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2701 others

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168194: contig of 14720 bp in length 168294: gap of 100 bp 182165: contig of 13871 bp in length 182265: gap of 100 hp
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+ ×	193366 314731; gap of 100 bp
JRES	Location/Qualifiers
source	1214721
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misc_feature	11080
	<pre>/note="assembly_fragment"</pre>
misc_feature	11813071
	<pre>/note="assembly_fragment"</pre>
min harman	2112

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 26 agccgagcatggaccgacccgactgcgactccacctgggaggaggacgaggaggatgcgg 85
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Rabbit calcium binding protein (calreticulin) mRNA,
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Rabbit (neonatal) skeletal muscle sarcoplasmic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecular cloning of the high affinity calcium-binding protein (calreticulin) of skeletal muscle sarcoplasmic reticulum J. Biol. Chem. 264, 21522-21528 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolac
1 (bases 1 to 1865)
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dichalak, 29-SEP-1989.
                                                                                                                                                                                                                                                                                                                    /protein_id="AAA31188.1"
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<1. .1865
                                                                                                                                                                   112. .1314
/note="calreticulin"
1 543 c 579 g
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WDERAKIDDPTDSKPEDWDKPEHIPDPDAKKPEDWDEEWDGEWEPPVIQNPEYKGEWK
PRQIDNPDYKGTWIHPEIDNPEYSPDANIYAYDSFAVLGLDLWQVKSGTIFDNFLITN
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                                                                                                                                                                                                                                             DEAY AEEFGNETWGVT KTAEKQMKDKQDEEQRLKEEEEEKKRKEEEEAEEDEEDKDDK
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92113549
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3 (bases 1 to 13680)
4 (Coeph.D.J., Cunningham,C., McIntyre,G. and Dolan,A.
Comparative sequence analysis of the long repeat regions and
adjoining parts of the long unique regions in the genomes of
simplex viruses types 1 and 2
J. Gen. Virol. 72 (Pt 12), 3057-3075 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Whitton,J.L., Rixon,F.J., Easton,A.J. and Clements,J.B. Immediate-early mRNA-2 of herpes simplex viruses types unspliced: conserved sequences around the 5' and 3' ter correspond to transcription regulatory signals Nucleic Acids Res. 11 (18), 6271-6287 (1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Davison, A.J. and Wilkie, N.M.
Nucleotide sequences of the joint between herpes simplex virus types 1 and 2
J. Gen. Virol. 55 (Pt 2), 315-331 (1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herpes simplex virus type 2 (isolate:HG52) DNA, clon
human herpesvirus 2
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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D10471.1 G1:221784
D10471.1 G1:221784
ICP0; ICP27; ICP34.5; RL1; RL2; Syn-associated membrane
glycoprotein; UL53; UL54; UL55; UL56; Vmw118; Vmw63; long repeat
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Herpes simplex virus
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                                                                                           /note="for UL53"
802. .806
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HPLFLTITTWCFVSIIALTELYFILRRGSAPKNAEPAAPRGRSKGWSGVCGRCCSIIL
SGIAVRLCYIAVVAGVVLVALRYEQEIQRRLFDL"
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                                     note="UL54 ORF"
                                                                        note="for UL54"
                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                 /note="UL53 ORF"
                                                                                                                                                                                                                                                                                                                    clone="f, p and g"
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/note="latency associated complement(7996. .8001)
/note="for RL2"
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RGGRLRCTGPFSCGTIKDVSGASPAGEYTINGIVYHCHCRYPFSKTCWLGASAALQHL
RSISSSGTAARAEQRRHKIKIKIKV"
3310...3315
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MALSLTPPHADGRAPVPERKAPSADTIDPAVRAVLRSISERAAVERISESFGRSALVM
                                                                  /product="Vmw118(ICP0)"
complement(10156. .1083)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(8251. .9974,10156. .10834,11242. .11316))
/note="RL2 ORF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="start of internal large repeat"
6594. .8808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="right extremity of long unique region" 4356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGSVGPADOPRVOSSETWRPPLVNSRELYRAQRAARCASSSDTPQAPGWCGGTCRHAV
FGVVAVVVVIILAFLWR"
4355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MALGAGHAHACRDDGDDSVIDAPPPYESVAGASAGQFVVIDIDT
PTDSPPPYSAGTSPVGLVSPASSGDGEVCERGRSRRAAWRAARRARRRAERRARRRSF
GPGGLFVETPLFLPEINIGAHPGVGGDLPSGLPTYAEATSDRPPTYAMVMAACPTEPP
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TAKAMRDCVLRQENLIEALASADETLAWCKMCIHHNLPLRPQDPIIGTAAAVLENLAT
RLRPFLQCYLKARGLCGLDDLCSRRRLSDIKDIASFVLVILARLANRVERGVSEIDYT
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complement(<11242. .11316)</pre>
                                                                                                                                           complement(<8251. .9974)
                                                                                                                                                                 GLRSRHPWSREQGAPAPAGDAPAGHGE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="UL56 ORF"
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/translation=""""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(3444. .4151)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="for UL56"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVGVGAGETMHFYIPGACMAGLIEILDTHRQECSSRVCELTASHTIAPLYVHGKYFYC
                                                                                                                                                                                          AAAPAWSRRTLLPEHARNCVRPPDYPTPPASEWNSLWMTPVGNMLFDQGTLVGALDFH
                                                                                                                   /number=3
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RESULT 1
HSV2HG52
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Best Local Similarity 62.0%;
Matches 103; Conservation
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s capsid associated tegument protein; capsid protein; complete genome; decxyribonuclease; decxyridine triphosphatase; DNA polymerase; envelope protein; glycoprotein B; glycoprotein C; glycoprotein D; glycoprotein E; glycoprotein G; glycoprotein H; glycoprotein I; glycoprotein J; glycoprotein K; glycoprotein H; glycoprotein I; glycoprotein J; glycoprotein K; glycoprotein H; glycoprotein M; host shut-off factor; integral membrane protein; minor capsid protein; membrane-associated phosphoprotein; minor capsid protein; membrane-associated phosphoprotein; minor capsid protein; neurovirulence factor; protease; protein kinase; ribonucleotide reductase large subunit; ribonucleotide reductase large subunit; ribonucleotide reductase small subunit; RL1 gene; UL10 gene; UL11 gene; UL12 gene; UL13 gene; UL13 gene; UL18 gene; UL19 gene; UL20 gene; UL20 gene; UL31 gene; UL32 gene; UL34 gene; UL35 gene; U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 9gacgcggaggacgaggactgcgaggacggcgaggcgcgcggcggagggacgcggggacgc 146
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0.74-0.84
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Herpes simplex virus type 2 (strain HG52), complete genome.
286099
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/APAGKYCFSPKYQVRHLYAWETAARLARRGSWARERADRDRFRRRVAAAEAVIGPCLE
/PEARARARARARAHEDGGPAEEEEAAAAARGSSAAAGPGRRAV"
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1 5124 c 4789 g 1893 t
genome % units.
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complement(13338, .13341)
/note="for RL1"
13365, .13618
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/note="RL1 ORF"
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/note="for RL1"
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complement(11474. .11478)
/note="for RL2"
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4 (bases 1 to 154746)
Barnett, B.C., Dolan, A., Telford, E.A., Davison, A.J. and McGeoch, D.J. A novel herpes simplex virus gene (UL49A) encodes a putative membrane protein with counterparts in other herpesviruses J. Gen. Virol. 73 (Pt 8), 2167-2171 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (08-DEC-1999) A. Dolan, MRC Virology Unit, Church Street,, Glasgow,, G11 5JR, UK
On Dec 13, 1999 this sequence version replaced gi:1869820.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 (bases 1 to 154746)
McGeoch,D.J., Cunningham,C., McIntyre,G. and Dolan,A.
Comparative sequence analysis of the long repeat regions a
adjoining parts of the long unique regions in the genomes
simplex viruses types 1 and 2
J. Gen. Virol. 72 (Pt 12), 3057-3075 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission Submitted (25-FEB-1997) A. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 154746)
Everett, R.D. and Fenwick, M.L.
Everett, R.D. and Fenwick, M.L.
Comparative DNA sequence analysis of the host shutoff genes of different strains of herpes simplex virus: type 2 strain HG52 encodes a truncated UL41 product
J. Gen. Virol. 71 (Pt 6), 1387-1390 (1990)
90278430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   viruses; dSDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Simplexvirus.

1 (bases 1 to 154746)

McGeoch, D.J., Moss, H.W., McNab, D. and Frame, M.C.

DNA sequence and genetic content of the HindIII I region in the short unique component of the herpes simplex virus type 2 genome identification of the gene encoding glycoprotein G, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Street,, Glasgow,, Gll revised bu [6]
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gene; UI50 gene; UI51 gene; UI52 gene; UI53 gene; UI54 gene; UI55
gene; UI56 gene; UI6 gene; UI7 gene; UI8 gene; UI9 gene; UI9 gene; UI9
glycosylase; US1 gene; US10 gene; US11 gene; US12 gene; US2 gene;
US3 gene; US4 gene; US5 gene; US6 gene; US7 gene; US8 gene; US8A
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J. Gen. Virol. 68 (Pt 1), 19-38 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human herpesvirus 2.
human herpesvirus 2
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                                                                                                                                                                                                                                    440. .1379
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/protein_id="CAB06759.1"
/protein_id="CAB06759.1"
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/tabslation="MSSRRGPRREGERREFREDEAPAVPRPGAPAVPRPGALPTADSQM
/translation="MSSRRGPREGEAPADSDDADYAGNDDAEWANSPPSEGGGKAP
VPAYDSGTAVESAPAASSLLRRWLLVPQADDSDDADYAGNDDAEWANSPPSEGGGKAP
EAPHAAPAAACPPPPPRKERGFQRPLPPHLALRLRTTTEYLARLSLRRRRPPASPPAD
                                                                                                                                                                                   join(440. .934,1089. .1379)
/gene="RL1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="HG52"
/db_xref="taxon:10310"
                                                                                                                                                           'codon_start=1
                                                                                                                                                                                                                                                                                           /number-1
                                                                                                                                                                                                                                                                                                                                                                    note="start"
                                                                                                                                                                                                                                                                                                                                                                                                                'note="a sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="human herpesvirus
                                                                                                                                                                                                                                                                                                                                                            of TRL (terminal copy of Long Repeat region)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dolan, MRC Virology Unit, Church
, UK
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9276. .9297
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                                                                                                                                                                                                                                                                                                                                                                                                                                            note="primary transcription associated transcripts (LAT's
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/note="proposed
LAT species)"
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943. .1070
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/gene="RL2"
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PEARARARARAHEDGGPAEEEEAAAAARGSSAAAGPGRRAV"
446. .460
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2303. .2377
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1738. .1743
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461. .547
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Search completed: October 12, 2000, 18:10:42 Job time: 35618 sec
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Best Local Similarity 62.0
Matches 103; Conservative
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VGRRDLRPANTTSTWEPPVSSDDEASSQSKPLATQPPVLALSNAPPRRVSPTRGRRRH
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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121.6	121.8	122	696.8	979	1352.6	1680.8	1688.8	2212.8	2256.6	2263.6	2348	Score
5.2	5. 2	5.2	29.7	41.7	57.6	71.6	71.9	94.2	96.1	96.4	100.0	% Query Match
161573	30752	162114	2208	1232	1676	6670	160241	2363	2423	2483	2423	Query Match Length
72	72	72	12	11	11	11	35	11	11	11	11	BB
AB021506	HHU92288	AF157706	AF156878	AF172449	AF172450	AF112980	HS885L7	AF172452	AF109134	AF172453	AF172451	ID
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ORGANISM
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Homo sapiens opioid growth factor receptor mRNA, complete cds.
AF172451 G1:7595302
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2agon, I.S., Verderame, M.F., Allen, S.S. and McLaughlin, P.J.
2agon, I.S., Verderame, M.F., Allen, S.S. and McLaughlin, P.J.
Direct Submission
Submitted (26-JUL-1999) Department of Neuroscience and Anatomy,
Submitted (26-JUL-1999) Department of Neuroscience and Anatomy,
Pennsylvania State University College of Medicine, 500 University
Drive, Hershey, PA 17033, USA
                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2423)
2 agon, I.S., Verderame, M.F., Allen, S.S. and McLaughlin, P.J.
Cloning, sequencing, chromosomal location, and function of cDNAs encoding an opicid growth factor receptor (OGFr) in humans
Brain Res. 856 (1-2), 75-83 (2000)
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alternatively spliced"
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ACO25920 Homo sapi
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ACO11899 Homo sapi
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AF112980 Homo sapi
U93872 Kaposi's sa
AL035669 Human DNA
AF172451 Homo sapi
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Direct Submission
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Zagon,I.S., Verderame,M.F., Allen,S.S.
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Direct Submission
Submitted (23-NOV-1998) Cell Biology, University of Birmingham, 1670 University Blvd. VH302, Room 605,
                                                                                                                                                      Liu,J., Brewton,R.G., Takanosu,M., Wood,B.M. and Mayne,R. Cloning of 7-60: A human gene from chromosome 20q13.3 which a novel intracellular protein motif repeated seven times
                                                                                                                           Liu,J.,
                                                                                                                                             Unpublished
                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 2423)
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                                                                                                                                                                                                                                                                  mRNA
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GPAGDEPAKTPSETPGPSPAGPAGDEPAESPSETPGPRPAGPAGDEPAESPSETPGPRPA
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Zagon, I.S., Verderame, M.F., Allen, S.S. and McLaughlir Cloning, sequencing, chromosomal location, and functioneoding an opioid growth factor receptor (OGFr) in brain Res. 856 (1-2), 75-83 (2000)
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Direct Submission
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FLPNGCFIEDILONWTDNYDLLEDNHSYIGWLFHLEDYBVKSS
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/note="[Met-5]-enkephalin
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                                           cggcagagtgccctggactacttcatgttcgccgtgcgctgccgacaccagcgccgccag
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HFRPRCKFVWGPDDKLKRFKESSLPHPLEGSKRVEERGSPGDPDHEASTQGRPCGPEH
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SPAGPTRDEPAEKAGEAAELQDAEVESSKKSGKP*

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1861 gcaggggacgagccagccgagagcccatcggagaccccaggcccccgccc	Qy
1801 acaagggatgagccagccgagagcccatcggagaccccaggccccggcccg 	Qу Дъ
1741 gcaggggacgagccagccgagaccccatcggagaccccaggcccagcccg	Qy Db
1665	da gy
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621 gcaggggacgagccagccgagagcccatcggagaccccaggcccccgccc	Qy
1561 cccaaagaaggtacccctgggagcccatcggagaccccaggccccagcccag	Qy Db
1501 caccccaaggctggacacagtgagaacggggttgaggaggacacagaaggtc 	Qy Db
441 GCGGTGG	д у .
381 AGGGTGGCCGACAAGGTGAGGAAGGGAAGGAAGGTGAGGGTGCTGCC	\$ B 1
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GEAAGATAGGCCGGAGCCCTTAAGCCCCCAAAGAAGAGCAAGAAGAAGAAGAAGAAGAAGA	d , b
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1081 gtggagccccaggatgcgggacccctggagaggagccagggggatgaggcaggg	Qy
1021 tgtgggccagagcatagcaagggttggggcagggtggacgaggggccccagccac 	Qy
961 gtggaggaggaaggaagcoccggggaccccgaccacgaggccagcaccagggt	Qy Qy
901 gacaagctgcggaggttcaagcccagctctctgccgcatccgctcgagggctccc 	\$ Q
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                                                                                                                                                                                                                              requests: clonerequest(sanger.ac.uk clone requests: clonerequest(sanger.ac.uk on Jul 8, 2000 this sequence version replaced gi:8919619.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggggggcg 2348
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http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr20 RP5-885L7 is from the library RPCI-5 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further
                                                                                                                   The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [] (bases 1 to 160241)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (09-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    details see http://bacpac.med.buffalo.
VECTOR: pCYPAC2
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6974 .7049
/note="4 copies 19 me
7224 .7451
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                    /note="AluY repeat: matches 5.
10876. .10962
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/note="12 copies 80 mer 61% conserved"
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/map="q13.2-13.33"
/clone="RP5-885L7"
                                                                                                                 'note="6 copies 38 mer 98% conserved"
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/note="443 (
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="L1MA9 repeat: matches 6210. .6254 of consensus"
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note="4 copies 34 mer 8.
note="2 copies 7.
19546. locies 7.
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/note="44 copies 6 mer aaagaa 62% conserved"

16664. 16885

/note="3 copies 74 mer 78% conserved"

/note="5 copies 47 mer 77% conserved"

/note="5 copies 47 mer 77% conserved"

16848. 16899

/note="13 copies 4 mer gaag 100% conserved"

17287. 17411
                                                                   /note="4 copies 20 n
19839 .19954
/note="2 copies 58 m
20020 .20103
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.o598. 16837
/note="5 cor/
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15824 . 15891
/note="17 copies 4 mer t.
16266 . 16577
/note="AluSq repeat: mat.
16578 . 16866
/note="17 copies 17 mer 6
/note="3
20710.
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18317. .18496
/note="3 copies 60 mer 7
18319. .18486
/note="7 copies 24 mer 6
18320. .18495
/note="44 copies 4 mer a
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1658s
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18497. 18546
/note="25 copies 2 mer ac 72% conserved"
19329. 19433
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/note="9 copies 18 mer
18327. .18486
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/note="10 copies 4 mer ccat 92% conserved"
18303. .18502
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14394. .14478
/note="5 copies 17 mer 77% of the copies 18 mer ctca
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/note="11 copies 16
                                      /note="MIR repeat: matches 20704. .20805
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16590. .16874
/note="15 copies 19 mer 64% conserved"
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/note="11 copies 24 mer 68% conserved"
16582. 16891
/note="10 copies 31 mer 66% conserved"
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16585. .16840
| note="16 copies 16 mer 66% conserved"
                                                                                                                                                                                                                      e="LTR16C repeat: matches 286. .387
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.18498
        3 copies
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   ggtggatgagggtgctggggacagtgctgcggtggccagtggtggtgcccagaccttggc
                                                                       gcagccctgccgccaacccctgggagccagggtggccgacaaggtgaggaagcggaggaa
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20722. 20806
/note="5 copies 17 m
21349. 21410
/note="2 copies 31 m
21584. 21654
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/note="MLT1D repeat: matches 107.
25853. .26065
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                                                                AF112980
Metazoa;
                                     GI:4139271
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Chordata;
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Craniata;
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Vertebrata;
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Euteleostomi;
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CCTGGTGCGGCGGGAGCTGCCGGGGGGGGGGCAGAGTGCCCTGGACTACTTCATGTTCGC

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CCCGGATCTCTCGCAGCGCAGCCACAACAACCTCCGCATCACACGCATCCTCAAGTCGCT 4934
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1 (bases 1 to 6670)
Takanosu, M., Liu, J. and May
Genomic Structure of Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 6670)
Takanosu, M., Liu, J. and
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/db_xref="taxon:9606"
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f Human Gene
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TAGAATTCAGCGGCCGCTGAATTCTAGCCGAGCATGGACGACCCCGACTGCGACTCCACC

60 60 Query Match
Best Local Similarity 98.
Matches 1364; Conservative

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Homo sapiens
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1 (bases 1 to 1676)

Zagon, I.S., Verderame, M.F., Allen, S.S. and McLaughlin, P.J.

Cloning, sequencing, chromosomal location, and function of cDNAs encoding an opioid growth factor receptor (OGFr) in humans

Brain Res. 856 (1-2), 75-83 (2000)
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Zagon, I.S., Verderame, M.F.,
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//protein_id="AAP64403.1"
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HERPRCKETWGDDKLREFKPSSLPHPLEGSRKVEEEGSPGDPDHEASTQGRTCGFEH
SKGGGRVDEGPQPRSVEPQDAGPLERSQGDEAGGHGEDRPEPLSPKESKRKLELSRR
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alternatively spliced"
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Zagon, I.S., Verderame, M.F., Allen, S.S. and McLaughlin, P.J.
Zagoning, Chromosomal location, and function of
encoding an opioid growth factor receptor (OGFr) in humans
main Res. 856 (1-2), 75-83 (2000)
                                                                                                                                                                                                                                                                                                                                                                                Pennsylvania State University
Drive, Hershey, PA 17033, USA
Location/Qualifiers
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Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
/chromosome="20"
/map="20[3],3"
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41.7%; 99.5%;

Score Pred.

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/db_xref="taxon:10116"
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Human herpesv with human he J. Virol. 73	TITLE JOURNAL MEDLINE
adjacent divergent open reading frames Arch. Virol. 142 (1), 193-204 (1997) 97300864 6 (bases 1 to 162114) Dominguez,G., Dambaugh,T.R., Stamey,F.R., Dewhurst	JOURNAL MEDLINE REFERENCE AUTHORS
Lindquester,G.J., Greenamoyer,C.A., A Pellett,P.E. and Dambaugh,T.R. Comparison of a 20 kb region of human human beta herpesviruses reveals cons	AUTHORS
Genetic content of 229 spanning the containing the or Arch. Virol. 142 97300856	JOURNAL MEDLINE
Arch. Virol. 141 (2), 367-379 (1996) 96195263 4 (bases 64106 to 84963) Lindquester,G.J., O'Brian,J.J., Anton,E.D., Gr Pellett,P.E. and Dambaugh,T.R.	JOURNAL MEDLINE REFERENCE AUTHORS
Dambaugh, T.R., O'Brian, J.J., Danovich, K.M., Frenk Pellett, P.E. Restriction endonuclease mapping and molecular cl Respessirus 6 variant B strain 229 genome	TITLE
95074921 3 (bases 64106 to 84963; 106012 to 126166) Lindquester, G.J., Inque, N., Allen, R.D., Castel	MEDLINE REFERENCE AUTHORS
Intragenomic suggests acq	TITLE JOURNAL
yilotogy L3 (4), 341 (3), 3331710 93331710 2 (bases 64106 to 84963) 2 (tamey, F.R., Dominguez, G., Blac	MEDLINE REFERENCE AUTHORS
A strongly immun variant B strain gene and mapping epitope	TITLE
22886) hez-Martinez,D., Dominguez,G., yer,C. and Dambaugh,T.R.	REFERENCE AUTHORS
	SOURCE
AF157706 162114 bp DNA VRL 2 Human herpesvirus 6B strain Z29, complete genome. AF157706 L13162 L14772 L16947 AF157706.1 GI:5733510	RESULT 10 AF157706/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS
ccctgcccatcggggcaccccaaggctggacacagtgagaacggggttgagga 	Qy 1485 Db 1506
tgctggggacagtgctgcggtggccagtggtggtggcccagaccttggcccttgccgggt	Qy 1425 Db 1452
ccaacccctgggagccagggtggccgacaaggtgaggaagcggaggaaggtggatgaggg 	Qy 1365 Db 1401
	Db 1369

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Submitted (10-JUN-1999) Herpesvirus Section, Centers for Disease
Control and Prevention, 1600 Clifton Road, Malistop G18, Atlanta,
GA 30333, USA
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9 (bases 1 to
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Submitted (26-JUL-1993) Herpesvirus Section, Centers
Control and Prevention, 1600 Clifton Road, Mailstop (
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Pellett, P.E., Dominguez, G., Dambaugh, T.R., Stamey, F.R., Dewhurst, S
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GCPEDTHGFARSPGDLMGEMNGDLGDEGETGEGGDNGEGE"
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join(583. .841,955. .2975)
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THAGVSCELLETVRDPWTAYPGVRMTLTVARAQYRLWPDARRQLRLHLYAGHPLGPWI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1624
                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAGGGCCTCCAGC 129244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAGGGCCTCCAGCAGAGCTTCCAGCAGAGTCTCTAGCAGAGCTTCCAGCAGGGCCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     agggatgagccagccaggccgagacctgca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ggggacgagccagccgagaccccatcggagaccccaggcccaggcccggcaggacctaca 1803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAGAGCCTTCAGCAGGGCCTCCAGCAGAGTCTCCAGCAGAGCCTCCAGCAGAGCCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ggggacgagccagccgagagcccatcggagaccccaggcctccgcccggcaggacctgca 1743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCAGAGCCTCCAGCAGAGCCTCCAGCAGAGCCTCCAGCAGGACCTCCAGCAGGGCCTCCA 129558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ggggacgagccagccgagagcccatcggagaccccaggcccccgcccagcaggacctgca 1683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACAGAGCCTCCAGCAGAGCCTCCAGCAGAGCCTCCAGCAGCAGCCTCCAGCAGCCTCCA 129618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agggatgagccagc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ggggacgaaccagccgagagcccatcggagaccccaggccccagcccggcaggacctaca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kosuge, H., Isegawa, Y. and Yamanishi, K. Nucleotide sequence analysis of a 30-kilobase-pair herpesvirus-6B (HHY-6B) genome and strain-specific major immediate-early genes
Virus Res. 52 (1), 1-14 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human herpesvirus 6.
Human herpesvirus 6.
Viruses; dsDNA viruses; no RNA stage; Herpesviridae;
Betaherpesvirinae; Roseolovirus.
1 (bases 1 to 30752)
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U92288.1 GI:2769711
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                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (07-MAR-1997) Virology, Research Institute for Microbial Diseases, Osaka University, 3-1 Yamada-oka, Suita, Osaka 565, Japa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98115230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 30752)
Kosuge, H., Isegawa, Y. and Yamanishi, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submission
                                                                                                                                    /gene="H74"
<1. .1281
/gene="H74"
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/function="replication, helicase-primase complex, similar to HHV6A
/note="part of helicase-primase complex, similar to HHV6A
volume to HTV6A
vol
                                                                                                                                                                                                                             /db_xref="taxon:10368"
                                                                                                                                                                                                                                                                                         /serotype="B'
                                                                                                                                                                                                                                                                                                                             /organism="Human herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                          Osaka University, 3-1 Yamada-oka,
                                                                                                                                                                                                                                                           'isolate="HST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30752
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0; Mismatches 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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M. Alexander

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/gene="H77"
3757. .6231
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//db_xref="01:2769712"
//db_xref="01:276971
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complement(1316..2065)
/gene="H75"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /Translation="MHRASANSLINSYSGSMMWRNQSSGRRPSKRLSDNEATILSTINS
/IGAEDMLSKHLISYLPPNNEBIDMIYPSEQIMTE IEMLHGHUNFFKQGTIHHALDS
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ILGDISNIINFILQSIDNSHYNRYVDMICTVGIVPFMRTTFTAPNLYNLLQQVSSKLI
HDIVRHKQNIYTPILLGLSSVJIPDFHNIK IFRDRNSSQISCGKNKKALAFFTYSTPV
VIRNLMLTTPLAHLSPELKKHNSLRRHQKMCQLLNTFPIKVLTTAKTDYVNKK IND
IEXEEKNSDAKKSLIKFLLNLSDSKSKIGIRDSVEGFIQEITPSIIDQNKLMLNRGQF
RRRSALDTGERDVRDLFKKQIIKCMEBQIQTOMBELFTLKTTNAMFERKSULHSLLR
TNNDCDRYNPDLDHDLENLSLSRALNIVQRLFETSVSIDDTRSVANSFERSOITPDTQV
ADKRIDQIWEMEYMTFTELKKNVNQGQEESITYSNYSIELLIVPFLRRLLNIYNLES
IPEEFIFISLGEILLATYESSKIKHYLRVYNELNQISEVYNLTQTHPENNEPIFDS
IPEEFIFISLGEILLATYESSKIKHYLRTYNAMFTOOL"
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TVGDDGIWFHLEDGTWINGLEYKTICEKELGFOGFIGIIIIDSEDTIQDELKLNFFOFK
RRLIHMKVDTPEEFMLGGLVFALENLFLKGSTHKKLJARLVLFPVLSVTKILENTCD
KLVCTLRHIFFNEHASSILHKVPPMIRUXNEMKNTHIEVLELYFNTKRSHNFINLSLE
SRQLQDSSLQVIQLATQFAQIFYSKNEDTSS"
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BBRF2, EHV1 55, VZV 53, HSV1
                                                                                           /Translation="MSISSLEGGRYDNKFILLNMSSAPKIELIVDKVASLSERRLEGRL
/ETANSLETION="MSISSLEGGRYDNKFILLNMSSAPKIELIVDKVASLSERRLEGRL
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ERSIQIOQKQDLSIYNNVISDIAERALGAVACKTKELPDLCESSVIVIDEAGVILRHI
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VLSALICDDVLSKYCEVDNNWIIFVNNKKCADHAFGDFLKHLEGVLEDGSVEETL
ITCHLKHIRNSSIGVISKIKASTVGFSGTYEKFVELLQSDLFIEKTSCEQTIHAYSFL
ITCHLKHIRNSSIGVISKIKASTVGFSGTYEKFVELLQSDLFIEKTSCEQTIHAYSFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .3757. .6231
/gene="H77"
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/note="similar to HHY6A U76, HCMY UL104, HVS gene 43,
BBRF1, EHV1 56, VZV 54, HSV1 UL6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(1974. .3962)
/gene="H76"
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/gene="H76"
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/gene="H75"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="helicase, helicase-primase complex"
/note="similar to HHY6A U77, HCMY UL105, HYS g
BBLF4, EHY1 57, VZV 55, HSY1 UL5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSV1 UL8"
SGLMFGGMYSFCCSEFTTPEVLMEIKNIKMPSIEFLESEMSRMSRDVQTVETDERYDF
GLVDDGLSDMDLLEIDPCGDPFFTRYSKLPLINSLSFEEISLLYTTFKDIFISRFAIL
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/db_xref="GI:2769713"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=
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/protein_id="AAC40327.1"
/db_xref="GI:2769715"
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/db_xref="GI:2769714"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene 44,
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SNLNNLRRQNSALVIDDSSETEMFENAGSFNEDLLATTILETL"
complement(10493. .11260)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MYAEERGYGSFDNVIQAYEQIISQSLHLKRFEFDNGCFIEFLAD
SGTCEFFSKGWISMIYWTSETDSMGSLIVDIGMDEGKCRTYRARGLLLCSKSITSISQ
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VNFFIIGVSRSWTFLNSICFVVISEPFKEKRQKSHHETKRNLEEQSHEDGIAPTSTTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="H79"
/function="F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="CB6RH"
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LEITHLKHVYKLVDNDRAHLTYHPSSDNYHAMSFLCKFFDVKYVILGHDPYPDGRGCG
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BKRF3, EHV1 61, VZV 59, HSV1
                                                                                                                                                                                                           complement(10493. .11260)
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/note="start-codon ggg; similar to HHV6A U80,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="H80"
9838. .10449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="H79"
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8179. .8406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAC40342.1"
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VVHLGTDKQLPQILYKKGLPRLVIKDEMGFISVLDNNVSKFVDVVNGQSFHLCTTVDY
                                                                                                                                                                                                                                                                                                                                                                                                        /transl_except=(pos:9838.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="CB5RH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LNYENDNFIAPHIVKALKNENTMLIF"
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    KVKAARMPFIGCNHFVRTNLFLTEHGKDPINWNILNE"
                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="H80"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGDEPRRSIQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VNGAVEGALSPCVSIDNHEDQQHDELDKRVYAQVGGVLGSPKPRSLESLLCVSKADLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAC40328.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="possible replication protein"
/note="similar to HHV6A U79, HCMV UL112,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="CB6RH"
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                                                                                                                                                                                           UL114,
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AUTHORS
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AB021506/c
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MEDLINE
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Query Match 5.2%;
Best Local Similarity 56.3%;
Matches 228; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCAGCAGAGCTTCCAGCAGAGCCTCCAGCAGCAGAGCCTCCAGCAGAGCC 16584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCAGCAGGGCCTCCAGCAGAGCCTCCAGCAGAGCTTCCAGCAGAGCCTCCAGCAGGGCC 16644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCAGCAAAGCTTCCAGCGAGTCTCTAGCAAAGCTTCCAGCAGGGCCCTCCAGAAGAGCC 16704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gccagccgagagcccatcggagaccccaggcctccgcccggcaggacctgcaggggacga 1751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gccagccgagagcccatcggagaccccaggcccccgcccagcaggacctgcaggggacga 1691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCAGCAGAGCCTCCAGCAGAGCCTCCAGCAGGGCCTCCAGCAGGGCCTCCAGCAGAGCC 16524
                                             Isegawa,Y., Mukai,T., Nakano,K., Kagawa,M., Chen,J., Mori,Y., Sunagawa,T., Kawanishi,K., Sashihara,J., Hata,A., Zou,P., Kosuge,H. and Yamanishi,K.
Comparison of the complete DNA sequences of human herpesvirus 6 variants A and B
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AB021506 161573 bp DNA
Human herpesvirus-6 (HHV-6), variant:B,
J. Virol.
99412319
                                                                                                                                                                                                                                                  Human herpesvirus 6 (strain:HST, pop_variant:B) DNA.
Human herpesvirus 6
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                       DNA, complete sequence AB021506
                                                                                                                                                                                               Betaherpesvirinae; Roseolovirus.
1 (sites)
                                                                                                                                                                                                                                                                                                                                                                        AB021506.1 GI:4995977
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/gene="H83"
12057. .12506
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/gene="H82"
/function="gH-gL complex, infection, cell fusion"
/function="gH; similar to HHV6A U82, HCMV UL115, HVS
/note="gL; similar to HHV6A U82, HCMV UL115, HVS
EBV BKRF2, EHV1 62, VZV 60, HSV1 UL1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(11336. .12088)
/gene="H82"
complement(11336. .12088)
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                        73 (10), 8053-8063 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 121.8; DB 72; pred. No. 1.2e-09; 0; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                strain:HST, virion
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Direct Submission
Submitted (18-DEC-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isegawa, Osaka University Medical School, Department of Microbiology; Ymada-oka 2-2, Suita, Osaka 565-0871, Japan (E-mail: Lsegawa@micro.med.osaka-u.ac.jp, Tel:81-6-879-3323,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax:81-6-879-3329)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 161573)
                                                                                                                                                                                                                 /gene="DR2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1027. .2970
/gene="DR2"
                /translation="MSRVFSCYLRACVCAGLCCWVCMGVIGGDCQRWWRRRCARWGRVGPRVLDGGAWRVRSGDGVRSVSSTCKTERAPSAARSPVZSPFYLVSSSSSSCSSACSSRCSSRVSSPHASHRVCAEGGRDLPMHGADGDADEGTDTLLEKGGADEGAGGNATGCPEDTRGFARSPGDLMGEMNGDLGDEGETGEGGDNGEGE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(2718. .3320)
/gene="DR3"
/note="82.5% identical to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="BAA78212.1"
/db_xref="GI:4995979"
/tabslation="kblarvshalhrlplshywwillgrhslrhvhsylrlhkglrl
/translation="kblarvshalhrlplshywwillgrhslrhvhsylrlhkglrl
plpwpeoeclhlhpkpykfilrypcltrophilogwpadssice"
                                                                                                                                                                                       VPSSASPSAPCIGRSRPPSAQTA"
complement(2718. .3320)
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/gene="LT1"
                                                                              /protein_id="BAA78214.1"
/db_xref="GI:4995981"
                                                                                                                                                                       /gene="DR3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTPLFLTPPGSLK"
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/gene="LT1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10368"
/pop_variant="B"
                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="DR1"
                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="68.2% identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="86.4% identical to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="HST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'organism="Human herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .161573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e="52.5% identical to LT1 gene of strain U1102 of
                                                                                                                                                                                                                                                                                                                                                                                                                                         gene family"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to the DDBJ/EMBL/GenBank databases. Yuji
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                                                                                                                            DR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DR2
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                                                                                                                            strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of strain Ul102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="DR7"
6512.
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7928 .8662
/gene="DR8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5025. .5336
/gene="DR6"
5025. .5336
                                                                                                                                                 /note="13.6% identical to HHV-6"
                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(7236. .7706)
/gene="DRHN2"
/note="ORF unique to HST
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MAAARLCRLASNUTEFARRGLQRDPVAYEEDLELPDRRMCGTNVRLEDVIAAAADEHDLLTVGGLCQTHAGVSCELLETVRDPWTAVEGVRWTLTVARRQYRLWPDARRQLKHLLYXAFHLGPWIVCAVLSREKETQTPSPPIGSGGVILGNVPTPGPREVEVETAWVIVTWRDRCYRSGPITARSAVWRTRSPPCGGWAAGHERTLDVFGPG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6512. .7150
/gene="DR7"
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VLGTSTAATVGGSVLPGADSYSRTVWTACREPGAATRSGHGLARGPIAPRRAGSRCVR
                                                                          complement(8292. .8807)
/gene="LJ1"
                                                                                                                                                                                                                                                                                                                                                                          /translation="MLAPPTPRGVYIKGECGALSSSPDLCDSPCRVGIGRCYSNSARG
RRCLTDRKYVFFLLCGVSNTERKHIVCDCVHSPILFLIGLKAGRDTVTRTYTHPTHTR
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/db_xref="GI:4995987"
                                                                                                                          complement(8292.
                                                                                                                                        CAPRPGSPHLPPPKNGRGYGGGWRVV"
                                                                                                                                                                                                                                                                                                                                                            RRIDISTAVLLFLFLRLRTPHFFFFVLYFEILVMIFLRSCLWPYIASLRLRRGV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(7236. .7706)
/gene="DRHN2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="transactivator"
/protein_id="BAA78217.1"
/db_xref="GI:4995984"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="3AA78216.1"
/db_xref="GI:4995983"
/translation="MTTRHTQMRDGRIAIRRDGARLAHARARARFEWLLLARGRPSKL
YGYTSRHRGERIHLPWPRYWCLELHPDPYRDARSATVWGHRWGWPPTHVRPRSVQDCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSSACVALS"
                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="BAA78218.1"
/db_xref="GI:4995985"
                                                             'note="16.6% identical toLJ1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="42.2% identical to DR7 gene of strain U1102 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    function="transforming activity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="DR6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="84.5% identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene family"
                                                                                                                            .8807)
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                                                             of strain U1102
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Matches 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aaagaaggtacccctgggagcccatcggagaccccaggccccagcccagcaggacctgca 1623
                                agggatgagccagccaaggc 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACAGAGCCTCCAGCAGAGCCTCCAGCAGAGCCTCCAGCAGAGCCTCCAGCAGAGCCTCCA 129434
   GCAGAGCCTCCAGCAGAGCC
                                                                                                                                                           ggggacgagccagccgagacccccatcggagaccccaggccccagcccggcaggacctaca 1803
                                                                                                                                                                                                                                                                                                                                                                                                                      GCAGAGCCTCCAGCAGAGCCTCCAGCAAGACCTCCAGCAGGGCCTCCAGCAGAGCCTTCA 129374
                                                                                                                                                                                                                                                                                                                                                                                                                                            ggggacgagccagccgagagcccatcggagaccccaggccccagcccagcaggacctgca 1683
                                                                                          ggggacgaaccagccgagagcccatcggagacccccaggccccagcccggcaggacctaca 1983
                                                                                                                                       GAAGAGCCTCCAGCAGGGCCTCCAGCAGAGCCTCCAGCAGAGCCTCCA
                                                                                                                                                                                                            GTAGGGCTTCCAGCAAAGCTTCCAGCGGAGTCTCTAGCAAAGCTTCCAGCAGGGCCTCCA
                                                                                                                                                                                                                                                                             GCAGGGCCTCCAGCAGGGCCTCCAGCAGGGCCTCCAGCAGCAGCAGGGCGTCCG 129254
                                                                                                                                                                                                                                                                                                                                                 GCAAGGCCTCCAGCAGAGCCTCCAGCAGAGCCTCCAGCAGCCTCCAGCAGGCCTCCA
                                                                                                                                                                                                                                                                                                                                                                         GCAGGGCCTCCAGCAGAGCTTCCAGCAGAGCCTCCAGCAGGGCCTCCAGCAGAGCCTCCA
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/gene="TI"
/note="25.6% identical to
HHV-6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="BAA78221.1"
/db_xref="GI:4995988"
/translation="MRRAPERAIDLSTDPRPISVMQIRTRTRTDMPTRPHRADCHVSE
SIHTHEKIHTRKYTQENTHTQKYTHKKIHTQKKIHTHKKIHTHKKIHTQKNTHTQKNTHTQKNT
HTKKYPHTKKYTHKKIHTHKKIHTHKKIHTKKNHFIYALFSQC"
complement(9467. .10768)
/gene="U2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(10891..12051)
/gene="U3"
complement(10891..12051)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="mcsQfcGrsvhfhfrgrrreyDstlevsnscsvlnvivDvyvr LPVILpLsfffffillILsriphrkKwfcRspflGiSSWSLASALCPSSCSFSAGRD LRCDAAVpevkwTafvrILVarpLsADDVrDfvSTfAGraLLSwpvGaelrfarsdm LRCDAAVpevkwTafvrILVarpLsADDVrDfvSTfAHCRLALSwpvGaelrfarsdm LGITQAELAKLSRGYGCCPGMDLTVIGVTIFAEVSALVLGECGEIYAFNGVFDDALFREEDYVSSKCLWETGASFFGGMSGVDDALAFAVSFDKALVPLP WPRGAFFEFAVPRRAEKRWRLIPGGGVAVVIGRFFGRGVTLPLLRRQRVLMDQVGRVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YQLSPHMVEREMSAVSCGASTVVRRDCEDTLRDGDAGVDTS'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AASLDGGAVVRLSDSFRAFLAMGVRKLFKNHRFPPGHLWTMQLPVTCVHAPVINLPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="BAA78222.1"
/db_xref="GI:4995989"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="U2"
/note="92% identical to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              referereter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 121.6; DB 72;
Pred. No. 6e-10;
0; Mismatches 199;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01102
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REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
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SOURCE
ORGANISM
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DEFINITION
ACCESSION
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AF015297
                                                                                                     BASE COUNT
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 Matches
                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                Local Similarity
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Human herpesvirus
AF015297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soergel, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF015297.1 GI:2343282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 4742)
                                                                                                     1772
Conservative
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196. .4698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="ie2hom"
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                4.7%;
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                Score 110.6; DB 7
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Mismatches

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Gaps

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DB 72;

Length 4742;

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Submitted (21-JUL-1997) Institut fuer Klinische und Molekulare
Virologie, Universitaet Erlangen-Nuernberg, Schlossgarten 4,
Erlangen D-91054, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human herpesvirus 6 (strain Uganda-1102).
Human herpesvirus 6 (strain Uganda-1102)
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identification of an human herpesvirus-6 homologous to the immediate-early 2 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Soergel, A., Schiewe, U., Fleckenstein, B. and Neipel, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Betaherpesvirinae; Roseolovirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytomegalovirus"
/codon critiar to
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                                                                                                         TMI I YAAT PIDFVGAVKTCNKYAKDNPKE I VLRVCSI I DGDNPISI YN PISKEFKSKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="IE2hom"
/protein_id="AAB67722.1"
/db_xref="GI:2343283"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Human herpesvirus
/db_xref="taxon:10370"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Human herpesvirus
AF015298
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Submitted (21-JUL-1997) Institut fuer Klinische und Molekulare
Submitted (71-JUL-1997) Institut fuer Klinische und Molekulare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soergel, A., Schlewe, U., Fleckenstein, B. and Neipel, F. Identification of an human herpesvirus-6 transcription homologous to the immediate-early 2 gene of human cytomegalovirus-evidence for an early/late gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Betaherpesvirinae; Roseolovirus.
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ergel, A., Schiewe, U.,
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FDDLIIPGLESEGLIIPESSNNIESNNVEEGSDGELKTLAEQKCKQGNDNDVIQSAMK
LSGLYCDADITHTQPLSDNTHQDPIYSQESRIFTKTIQDPRIVAQTHRQCTSSASNLQ
SNESGSTQVREASELPNQLLQEMYTSHAQNANLQNNFTSLFYQPYRDDFYRDIESSYRE
SRNTNRGYDYNEFRHHPYRPRGROKYNYYNPNSKYQQPYKRCFTRTYNRRGRGHRSYD
CSDRTNRGYDYNEFRHTYPPYRPRGROKYNNYKDFTQLTMKFNFESYDYSMAFSTDSTHY
QSDNYNHPTKAQTIPETTKTKKHEATKDNETSTENQVLTPDVISLSYRPSSYKMDIIK
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D-91054, Germany
                                                                                                                                   /product="IE-2 protein"
/protein_id="AAB69858.1"
/db_xref="Gi:3384715"
/translation="MEPAKPSGNNMGSNDERMQDYRPDPMMEESIKEILEESIMCDTS
                                                                                                                                                                                                                                /gene-"ie2hom"
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/strain="Uganda-1102"
/db_xref="taxon:10368"
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KEYWORDS SOURCE

ORGANISM

Human herpesvirus 6.
Human herpesvirus 6
Viruses; dsDNA viruses,

Betaherpesvirinae; Roseolovirus.

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PNITVSEAFKMNHAPPKYYDKDEIKRFIQLQKQGPQELWDKFENNTTHDLFSRHSDVK
TMIIYAATPIDFVGAVKTCNKYAKDNPKEIVLRVCSIIDGDNPISIYNPISKEFKSKF
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gene
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                                                                                                                  polyA_signal
                                                                                                                                                                                                                                                                                                           polyA_signal
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Center, Johns Hopkins University, 418 North Bond Street, Baltimore,
MD 21231, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               음물
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence analysis of a 21-kbp region of the genome of human herpesvirus-6 containing homologues of human cytomegalovirus major immediate-early and replication genes
Virology 204 (2), 738-750 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 21191)
Nicholas, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95027704
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         LVRDLHMFYLTCDGKDTHVVMPLLQTAVENCWEKTTEIKQRPTFQCAEISRCGFIVYA
RFFLSSGLSQSKEAHWTVTASKYLSACIRTNKTGLCFASITVYFQDMMCVFIANRYNV
SYWIEEFDPNDYCLEYHEGLLDCSRYTAVMSEDGQLVRQARGIALTDKINFSYYILVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITRQQSLDQESLNETEVTRKETMLWDLQEQSNMMDKKIAAISNLIMNNGELVRTLSKF
FYPLTYVLGDDGLEILEAYVGGEELMLEDDYVPVILRCIGDYAALDYKHILLSNECTQA
SKKIREGYSYMDEHFSLIVSDYKICFSHTDYGEAVCEMKQIFSFSVCAFGGEQVLLV
TPKNAYALLFDDDLCLLLLQSVFAFLHEKIFGVYKQVLVQLCEYIGPDLWFFGNERSV
SFIGYVNLWLLSVSDLERRVPDYTYICREILSFCGLAFILGERGHAVPVVRELSIEM
PGSETSLQRERENGQYVSSESLCFOTQFEDTHLFFSDSDMYVYTLPDCLRLLLKSTYD
KAFLPCFDENATEIDLLLKFMSRLQHRSYALFDAVIFMLDAFVSAFQRACTLMGMRWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="HDRF1"
/note="component of helicase-primase complex; similar HCMV UL102 Swiss-Prot Accession Number P16827"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene=":
1949. .
                                                                                                                      /gene="HDRFO"
3790. .3795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RKQTIYKLQGSDISLSVSEVGVFGQHASPGVCVSS" 1949. .3937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDEYFYLGDISGYYEWGMLIDLAFLAEMIRKDLKLKSCTDTTTDISEDDLLLCAARRS
SDILQIMQLVFTVHVQFFQKYSLQTLQLFNKLRGMRIVTGVFSIEKFSISILRLFFKC
AFNMTLSASRPRYIPGKAYRNLTKNDMENMLDNWEISRTNLKTCKELRKALTEASRAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YMNOVLIRSYDPLADIAIPOSDWSVAEQSIISESCIDFRGKCSGAHKYNFCSVLKSL
FRYRHYIEKTTITSLSDSLFLKCSLLCENSIKVDIVGNGFPMRREVFLSFLQIILVBEC
HFIEKKITLDGDDMTFQEIISSRFTLNNGDFYENGDOLHKDYITDMGKFRATFILSFG
VDIFIASDIVYDLKNESKRYVFVNVWLQKCVSAGVESTEIERVFCERIKCYMLPKSFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NSSHVIAMDATLTRHVVEFFAAFKPDTQIALIRNTFVSAMFSNRIAYFCDTFFGKEFS
FFARLEDKLRWDKKLCLFCSTVLAAEYMYDLIRSRFPLKKVLLLTSKQGKCSSIESWI
RYDVVIYTSVVTVGLSFEPVYFSSLFVYIQLAKGGPDMVSVFQSIGRVRRVIDEDIYI
/gene="HDRFO"
/evidence=not_experimental
complement(3939. .4721)
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/db_xref="GI:662096"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Human herpesvirus
/strain="U1102"
                                                                                                                                                                                                                                                                                                                                                        CRVLRRWVESKFEDVEQTQFIRWENRMLCEHIHLLHLN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="G1:662097"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="SLHRLTENYDVLILDEIMSIIKQFYSKTMTKTKEVDCKFLSLIk/
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/map="109-130 kbp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /specific_host="Homo sapiens"
/db_xref="taxon:10368"
                                                                                                                                                                                                                                 evidence-not_experimental
                                                                                                                                                                                                    .3795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HDRF1"
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                                                                                                                                                                                                                                 polyA_signal
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/db_xref="G1:662100"
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ERSIQIQQKQDLSIYMNVISDIADRALGAVACKTKELPDLCESSVIVIDEAGVILRHI
LHTVVFFYWFYNALYKTPLYEDGIVPCIVCVGSDTQSNALVTSNPLTQNKDVKRGID
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VLSALICDDVLSKYCEVDNNNIIFVNNKRCADHAFGDFLKHIEFELPIXPELITYVDQ
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TLVCTLRHIFFXBEHASEILHKVPLMIRLYNEMKNTHIEVLELYENTKRSHNFINLSLE
SRQLQDSSLQVIQLATQFAQTFYSKNGDTSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FVKPASYIRNPMNEIETTRLFLSHNEVKNYFRSLHEQVEVTNRNNLFVFPVYFLIKNK
TFEDYKSEIGNFSLEIEPWFKSNIHRLNTYSQFADQDLSKTVQLEEIVLEDGSVEETL
ITCHLKHIRNSSIGVTSKIKASTVGFSGTYEKFVELLQSDLFIEKTSCDQTIHAYSFL
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complement(3939. .3944)
/gene="HDLF2"
                                                                                                          /evidence=not_experimental complement(9325. .10351)
                                                                                                                                                                                                                             ATVSKVSMTITKSQGLSIQKVAIDFGSDPKNLKLSSIYVGMSRVTDPNNLIMNVNPLR
LNYENDNFIAPHIVKALKNENTMLIF"
complement(9325. .9330)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="putative helicase; similar to HCMV UL105, Swiss-Prot Accession Number P16736"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="HDRF2"
6413. .8887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TUNDCDRYNPULDHDLENLSLSRALNI VQRLPFTSVSIDDTRSVANSFFSQYIPDTQY
ADKRLDQLWEMEYMRTFRLRKUVNQCQEESITY SUVSIELLI VPFLRRFLNI YNLES
IPEEFLFLSLGEILLAI YESSKIKHVLRLVYVRELNQI SEVFULTQTHPENSEPIFDS
NIFSPNPENEILEKIKRI RULRRIQHLTRPNYPKGDQD"
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IEKEEKSSDAKKSLIKFLLNLSDSKSKIGIRDSVEGFIQEITPSIIDQNKLMLNRGQF
RKRSAIDTGERDVRDLFKKQIIKCMEEQIQTQMDEIETLKTTNQMFERKIKDLHSLLE
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Number L14772"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence=not_experimental
complement(3939. .6618)
/gene="HDLF1"
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VVHLGTDKQLPQILYKKGLPRLVIKDEMGFISVLDNNVSKFIDVVNGQSFHLCTTVDY
                                                                                                                                                                                                                                                                                                                                                                                                                              SGLMFGGMYSFCCSKFTTPEVLMEIKNIKMPSIEFLESEMSRMSPDVQTVETDERYDF
GLVNDGLSDVDLLEIDPCGDPFFTRYSKLPLINSLSFEEISLLYTTFKDIFISRFAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(4630. .6618)
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/db_xref="GI:662098"
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                                                                                                                                                                                        /gene="EDLF5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="HDRF2"
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                                                                         'gene="EDLF5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .9409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Swiss-Prot Accession Number
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Query Match 4.2
Best Local Similarity 50.8
Matches 234; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               19400 GAGCCTCCAGCAGAGCCTCCAGCAGGGATTCTAGCAGAGCCTCCAGTAGAGCCTCCAGCA 19341
19160 GGGATTCTAGCAGGGCCTCAAGTAAAGCCTCAAGAAAAGCCTCCAGCAGAGCCTCCAGCA 19101
                                                                                                                        19220
                                                                                                                                                                                                                           19280 GGGATTCTAGCAGGGCCTCAAGCAAAGCCTCCAGCAGAGCCTCCAGCAGGGATTCTAGCA 19221
                                                                                                                                                                                                                                                                                                                                                19340 GGGCCTCAAGCAAAGCCTCCAGCAGAGCCTCCAGCAGAGCCTCCAGCAGCCTCCAGCA 19281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19460 GGGATTCTAGCAGGGCATCAAGCAGAGCCTCCAGCAGCCTCCAGCAGGGATTCTAGCA 19401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19520
                                                1903 ccccgcccggcaggacctgcaggggacgaaccagccgagagcccatcggagaccccaggc 1962
                                                                                                                                                   1843 ccccgcccggcaggacctgcaggggacgagccagcggagacccatcggagaccccaggc 1902
                                                                                                                                                                                                                                                                                                1783
                                                                                                                                                                                                                                                                                                                                                                                    1723 ctccgcccggcaggacctgcaggggacgagccagcgagaccccatcggagaccccaggc 1782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1603 cccagcccagcaggacctgcaggggacgagcccagccgagagcccatcggagaccccaggc 1662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1543 acagaaggtcgaacggggcccaaagaaggtacccctgggagcccatcggagaccccaggc 1602
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                                                                                                                                                                                                                                                                  cccagcccggcaggacctacaagggatgagccagccgagagcccatcggagaccccaggc 1842
                                                                                                               GAGCCTCCAGCAGGGATTCTAGCAGGGATTCTAGCAGGGCCTCCAGCAGAGCCTCCAGCA 19161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ccccgcccagcaggacctgcaggggacgagccagccgagagcccatcggagaccccaggc 1722
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VNFYFSCVTVVDFFLNSICFYAISELFKEKRQKYHDMKRNLEEQSHEDGITLTSTTLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="putative phosphoprotein; similar to HCMV UL113, Swiss-Prot Accession Number P17151"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"putative phosphoprotein; similar to HH6 CB7R, GenBank Accession Number L14772 and HCMV UL112, Swiss-Prot Accession Number P16768"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12483. .13180
/gene="EDRF2"
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complement(10022. .10351)
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11477. .12511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.2%;
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Db 19100 GGGCTTCCAGCAGGCCTCAAGCCAAAGCCTCCGGTAAAGCC 19060

Search completed: October 12, 2000, 18:33:21 Job time: 36977 sec

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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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GenEmbl:*

1: gb_bal:
2: gb_bal:
3: gb_ow:*
4: gb_bat:
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6: gb_pl:
7: gb_pl:
10: gb_pl:
11: gb_pl:
11: gb_pl:
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11: em_
11: em_
21: em_
22: em,
23: em,
23: em,
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23: gg
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93: gb_sts2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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44.5	59.0 42.7 30.5	5 100.0 2363 5 96.7 2423 4 93.9 2483 8 93.1 2423 8 68.5 160241 5 67.9 6670	% Query Match Length DB
72 72 72	1211	3 11 AF172452 3 11 AF172451 3 11 AF172453 3 11 AF109134 1 AF109134 1 35 HS885L7 0 11 AF112980	h DB ID
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Direct Submission
Submitted (26-JUL-1999) Department
Pennsylvania State University Colle
Drive, Hershey, PA 17033, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cloning, sequencing, chromosomal location, encoding an opioid growth factor receptor (Brain Res. 856 (1-2), 75-83 (2000) 20143540
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/product="opioid growth factor receptor"
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                                                                                         binding protein;
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AC012179 Homo sapi
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AF10917 Homo sapi
AF109189 Homo sapi
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GCGCCACTGGTCCGCTTCTTCCTGGAGGAGGACGCTGCCGGCGGGAGCTGCCGGGGGTG
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SEEPRAARPSSRQSRWIGSRWARATROMCRYRHBYPDLYERDCNODTPHLSFYRNBIR

FLPNGCFIEDILQNWYDNYDLLEDNHSYIQWLFPLREGVUNHAKPLITLREVEVRKS

QEIQERLYRAYELMLGFYGIRLEDRGTGYLGRAQNYQKREQULWRRSHNNLRITRLIK

SPCELSLEHFQAFLYRFLEFTLYRRELFGVROSALDYEMFAVRCHQRRQLYHBAWE

HFRPRCKFYWGPQDKLRRFKPSSLPHPLEGSKVEEEGSPGDPDHEASTQGRTCGPEH

SKGGRWDEGPOPRSVEPQDAGFLERSQGDEAGGHGEDRPEPLSFKESKRKLELSRR

EQPFTERFOPGAFSVENIALNLEGCALSQGSLRTGTOWGGODDEEAVQPCROFUGAR

VADKVRKRKVDEGAAGDSAAVASGGAQTLALAGSDAPSGHPKAGHSENGVEEDTEGRT

GPKEGTPGSPSETFGFSPAGPAADEPAESPSETFGFRPAAGPAGDEPAESPSETPGFSP

AGPTRDEPAESPSETFGFPRAGPAGDEPAESPSETFFGPRPAGPAGDEPAESPSETFGFPSP

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Homo sapiens |
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Zagon, I.S., Verderame, M.F.,
Direct Submission
Submitted (26-JUL-1999) Depa
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Drive, Hershey, PA 17033, USi
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhir
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Zagon, I.S., Verderame, M.F., Allen, S.S.
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alternatively spliced"
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1860	caqqqqacqaqccaqccqaqaqcccatcqqaqaccccaqqccccqccqqcaqqacc	œ	Qy
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1800	aagggatgagccagccgagagcccatcggagaccccaggccccgcccg		VΩ
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1740	cccatcggagaccccaggccccagccggcaggacc	1704	Qy
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1680	GCAGGGGACCAGCCGAGACCCCATCGGAGACCCCAGGCCCCAGCAGGACCT	1621	Db
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1620	CCCAAAGAAGGTACCCCTGGGAGCCCCATCGGAGACCCCAGGCCCCAGGCCCAGGACCT	1561	Дb
1620	ccaaagaaggtacccctgggagcccatcggagaccccaggcccagcccagcaggacc	1561	Qy
1560	CACCCCAAGGCTGGACACAGTGAGAACGGGGTTGAGGAGGACACAGAAGGTCGAACGGGG	1501	당
1560	accccaaggctggacacagtgagaacggggttgaggaggacacagaaggtcgaacggg	1501	Qy
1500	CGGTGGCCAGTGGTGCCCAGACCTTGGCCCTTGCCGGGTCCCCTGCCCCCATCGGG	1441	Db
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1440	AGGGTGGCCGACAAGGTGAGGAAGCGGAGGAAGGTGGATGAGGGTGCTGGGGACAGTGCT	iω	Db
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1380	apt gygog toaygacoctygygagycagtycagcoctgoogocaacocctgggago	1321	Qy
1320	ATCGCTCTGAATTTGGAGGGGTGTGCCCTCAGCCAGGGCAGCCTCAGGACGGGGACCCAG		망
1320	tcyctctyaatttygagggtytyccctcagccagggcagcctcaggacggggaccca	io.	Ωy
1260	AGCCGGCGGGAGCAGCCCACAGAGCCACGAGGCCCTCAGAGTGCCTCAGAGGTGGAGAAG	.20	Дb
1260	gccggcgggggagcagccgcccacagagccaggccctcagagtgcctcagaggtggagaa	N	Qy
1200	GGGGAAGATAGGCCGGAGCCCTTAAGCCCCAAAGAGAGAAGAAGAGAAGAGGCTGGAGCTG	1141	ДD
1200	ggggaagataggccggagcccttaagccccaaagagagcaagaagaggaagctggagct	\vdash	Qy
1140	GTGGAGCCCCAGGATGCGGGACCCCTGGAGAGGGAGCCAGGGGGGATGAGGCAGGGGGCCAC	1081	Dβ
1140	tygaycoccaggatycgggacccctggagaggagccagggggatgaggcagggggcca	1081	Qy
1080	TGTGGGCCAGAGCATAGCAAGGGTGGGGGCAGGGTGGACGAGGGGCCCCAGCCACGGAGC	1021	Дb
1080	gtgggccagagcatagcaagggtggggggcagggtggacgaggggccccagccacggag	1021	Qy
1020	GTGGAGGAGGAAGCCCCGGGGACCCCGACCACGAGGCACCAGGGTCGGACC	961	Db
1020	gtggaggaggaaggaagccccggggacccccgaggccaccac	ര	Qy
960	GACAAGCTGCGGAGGTTCAAGCCCCAGCTCTCTGCCGCATCCGCTCGAGGGCTCCAGGAAG	901	Db
960	acaagctgcggaggttcaagcccagctctctgccccatccgctcgagggctccaggaa		Qy
900	. CTGGTGCACTTCGCCTGGGAGCACTTCCGGCCCCGCTGCAAGTTCGTCTGGGGGCCCCCAA	841	Дb
900	ggtgcacttcgcctgggagcacttccggccccgctgcaagttcgtctgggggccc	841	Qγ

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DEFINITION
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(bases 1 to 2483)
Zagon, I.S., Verderame, M.F., Allen, S.S. and
Cloning, sequencing, chromosomal location,
encoding an opioid growth factor receptor of the second second
                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 2483)
Zagon,I.S., Verderame,M.F., Allen,S.S.
Direct Submission
Submitted (26-JUL-1999) Department of Pennsylvania State University College Corive, Hershey, PA 17033, USA
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Mammalia; E
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/db_xref="GI"7595307"
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/db_xref="taxon:9606"
/chromosome="20"
/map="20q13.3"
QEIQERLVRAYELMLGFYGIRLEDRGTGTVGRAQNYQKRFQNBNWRSHNNLRITRILK
                                                                                                                                                      alternatively
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                                                                                                                                              /note="[Met-5]-enkephalin
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HFRPRCKFVWGPQDKLRFKESSLPHPLEGSRKVEERGSPGDPDHEASTQGRRCEPEH
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Query Match 93.1
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1 (bases 1 to 2423)

Liu, J., Brewton, R.G., Takanosu, M., Wood, B.M. and Mayne, R.

Cloning of 7-60: A human gene from chromosome 20q13.3 which
a novel intracellular protein motif repeated seven times
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ADKVRKRRKVDEGAGDSAAVASGGAQTLALAGSPAPSGHPKAGHSENGVEEDTEGRTG
FKEGTPGSPSETPGPSPAGPAGDEPAESPSETPGPPRAPAGPAGDEPAESPSETPGPPRA
GPAGDEPAKTPSETPGPSPAGPTRDEPAKAGEAAELQDAEVESSAKSGKP*
PAGPAGDEPAESPSETFGPSPAGTTRDEPAKAGEAAELQDAEVESSAKSGKP*
BAGPAGDEPAESPSETFGPSPAGTTRDEPAKAGEAAELQDAEVESSAKSGKP*
BAGPAGDEPAESPSETFGPSPAGTTRDEPAKAGEAAELQDAEVESSAKSGKP*
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TITLE
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On Jul 8, 2000 this sequence version replaced 91:8919619.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:. EMBL; Sw:. SWISSPROT; Tr., TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/chr20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (09-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human DNA sequence from 20q13.2-13.33, complete
                                                http://www.sanger.ac.uk/HGP/Chr20
RP5-885L7 is from the library RPC1-5 constructed at the Roswell
Park Cancer Institute by the group of Pieter de Jong. For furth
details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 160241)
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s sequence is the entire insert of clone RP5-885L7 The true left of clone RP4-563E14 is at 140192 in this sequence. The true
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4317. .
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/note="12 copies 80 mer 61% conserved"
                                                                                                                                                                                                                        /note="L1M4 repeat: 6974. .7049
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65. .353
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5934. .6864
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                                                   /note="MIR repeat: 11974. .12025
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7224. .74
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4456. .5148
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/clone="RP5-885L7"
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                                                                                     /note="AluY repeat:
10876. .10962
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                                                                                                                                               18497. .18546
/note="25 copies 2 mer ac 72% conserved"
/19329. .19433
/note="LTR16C repeat: matches 286. .387 of consensus"
/19455. .19590
/note="4 copies 34 mer 88% conserved"
/19457. .19604
/note="2 copies 74 mer 81% conserved"
/19464. .19625
/note="4 copies 20 mer 76% conserved"
/19839. .19954
/note="2 copies 58 mer 87% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="4 copies 48 mer 67% conserved"
18317. .18496
/note="3 copies 60 mer 74% conserved"
18319. .18486
/note="7 copies 24 mer 66% conserved"
18320. .18495
/note="44 copies 4 mer acac 64% conserved"
18321 18406
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20710. .20811
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/note="17 copies 4 mer tccc 67% conserved"

16266. .16577

/note="AluSq repeat: matches 1. .313 of consensus"

16578. .16866
                                  /note="2 copies 51 mer 90% conserved" 20722. .20806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="14 copies 6 mer aaagaa 62% conserved"
16664. 16885
/note="3 copies 74 mer 78% conserved"
16670. 16904
/note="5 copies 47 mer 77% conserved"
16848. 16899
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/note="8 copies 20 mer 66% conserved"
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/note="9 copies 18 mer 66% conserved"
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/note="5 copies 40 mer 66% conserved"
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/note="3 copies 80 mer 77% conserved"
                                                                                                                  20020. .20103

"note="MIR repeat: matches 51. .137 of consensus"
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[6583._16879
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note="7 copies 40 mer 67% conserved"
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Le="5_copies 48 mer 73% conserved"
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Mammalia; Eut
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Zagon, I.S., Verderame, M.F., Allen, S.S. and McLaughlin, P.J.
Cloning, sequencing, chromosomal location, and function of
encoding an opioid growth factor receptor (OGFr) in humans
action Res. 856 (1-2), 75-83 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pennsylvania State University Drive, Hershey, PA 17033, USA
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Direct Submission
Similarity 99.4
31; Conservative
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clone 127
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Score 977.4;
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AF156878 2208 bp n
Rattus norvegicus opioid
AF156878
AF156878.1 GI:6693831
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Query Match 30.5
Best Local Similarity 70.0
Matches 1046; Conservative
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Mammalia; Eutheria;
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Nuclectide sequence analysis of a 30 kilobase-pair region of herpesvirus-6B (HHV-6B) genome and strain-specific variations major immediate-early genes
Virus Res. 52 (1), 1-14 (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="H4"
/function="replication, helicase-primase
/note="part of helicase-primase complex,
U74, HCMY UL102, HVS gene 41, EBV BBLF3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="H74"
<1. .1281
                                                                                                                                                                                                                                                 /translation="Losveaflhekifgvykqvlvqlceyigpdlwpfgnersvsfig
rpnukilsvsblerkvpdtyyigcreilsfcglapilgprghilpvlrelsvempgse
TSLQRFRFNSQVYSSESLCFQTgpebThlffeSbDiMyVTLPDCLTLLKSTVPRAFL
PCFDENATEIELLLKEMSRLQHRSYALFDAVIFMLDAFVSAFQRACTLMEMRWLLVRD
LHVFYLTCDGKDSHVVMPLLQTAVENCWEKITEIKQRPAFQCMEISRCGFVFYARFFL
SSGLSQSKEAHWTVTASKYLSACIRANKTGLCFASITYYFQDMMCVFTANRYNSYWI
                                   /product="H75"
/protein_id="AAC40325.1"
/db_xref="GI:2769713"
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/gene="H75"
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RRWVESKFEDVEQTEFIRWENRMLYEHIHLLHLN"
                                                                                                                                                                                                                                                                                                                                                              /product="H74"
/protein_id="AAC40324.1"
/db_xref="GI:2769712"
/translation="mkslkklkeletsdvfntlhvrtilkvikidkcvslarhslvni
TVGDDGIWFHLEDGTMINGLEYKTICEKELGFQGFIGIIILDSEDTLQELRLNPFQFK
                                                                                                                                                                              /gene="H75"
                                                                                                         /note="similar to HHV6A U75,
BBRF2, EHV1 55, VZV 53, HSV1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10368"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
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ILGDISNIINBTIGSIDNSHYNRXYDWAIGTUGHTPFMRTTPTAPNLYNLLGVYSKLI
HDIVRHKQNIYTPILLGLSSVIIPDFHNIKIFRRNSEQISGFKNKKAIAFTYSTFY
VIRNBLMLTTPLAHLSPELKHINSLRRHQKMCQLLNTFPIKVLTTAKTDYTNKKIMDM
IEKEEKNSDAKKSLIKFILNLSDSKSKIGIRDSVEGFIQEITPSIIDQNKLMLNRGQF
RKRSAIDTGEBDVRDLFKKQIIKCMEEQIQTQMDEIETLKTTNOMFERKIKDLHSLLE
TNNDCDRYNPDLDHDLENLSLSRALNIVQRLPFTSVSIDDTRSVANSFFSQYIPDTQY
ADKRIDQLMEMEYMRTFRLKNVNNQGQESITYSNYSIELLIVPFLRRLLNIYNLES
IPEEPLFLSLGEILLANISSSKIKHYLRLYVRELNQISEVYNLTQTHPENNEPIFDS
NIFSPNPENEILEKIKRIRNLRRIQHLTRPNYPKGDQD"
3757..6231
3757..6231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3757. .6231

/gene="H77"
/function="helicase, helicase-primase complex"
/note="similar to HHV6A U77, HCMV UL105, HVS gene 44,
BBLF4, EHV1 57, VZV 55, HSV1 UL5"
/codon_start=1
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VLSALICDDVLSKYCEVDNWIIFVNIKRCADHAFGDFLKHIEFGLPLKPELIEYVDQ
FVKPASYIRNPMREIEFTREFLSHNEVKNYFRSLHEQVEYNANLLFVPPVYFLIKNK
TFEDYKSEIGNFSLEIEPWFKSNIHRLNTYSQFADQDLSKTVQLEEIVLEDGSVEETL
TTCHLKHIRNSSIGVTSKIKASTVGFSGTYEKFVELLQSDLFIEKTSCCEQTIHAYSFL
SGLMFGGNYSFCCSETTFEVLMEIKNIKMFSIEFLESMKRMSRDVGTVETDERYDF
GLVDDGLSDMDLLEIDPGGDFFTRYSKLPLTNSLSFEEISLLYTTFKDIFISRFAIL
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6495. .6722
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ERSIQIQQKQDLSIYWNVISDIAERALGAVACKTKELPDLCESSVIVIDEAGVILRHI
ERSIQIQQKQDLSIYWNVISDIAERALGAVACKTKELPDLCESSVIVIDEAGVILRHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(1974. .3962)

'gene="R'76"

/function="possible virion protein"

/function="possible virion protein"

/note="similar to HHY6A U76, HCMV UL104, HVS

BBRF1, EHV1 56, VZV 54, HSV1 UL6"
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GGGLDGVLSINRSSFIFCTTEVILGIGVRIR"
8179. .8406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6495
                                  /translation="MLHNVSKCIHSICIRVCIKLHVICSSRFSIRCFAVYETYSLIPNTSDGRQAFLYAFYGKVHALVADAIRKGFRFG"
                                                                                                                                                                                                                              /gene="CB6RH"
8179. .8406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VYHLGTDKQLPQILYKKGLPRLVIKDEMGFISVLDNNVSKFVDVVNGQSFHLCTTVDY
ATVSKVSMTITKSQGLSIQKVAIDFGSDPKNLKLSSIYVGMSRVTDPNNLIMNVNPLR
LNYENDNFIAPHIVKALKNENIMLIF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRQLQDSSLQVIQLATQFAQIFYSKNEDTSS" complement(1974...3962)
                                                                                        /product="CB6RH"
/protein_id="AAC40343.1"
/db_xref="GI:2769731"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRLIHMKVDTPEEFMLCGLVFALENLPLKQSTLHKLIARLVLFPVLSPVTKILFNTCD
KLVCTLRHIFFNEHASEILHKVPPMIRLYNEMKNTHIEVLELYFNTKRSHNFINLSLE
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=]
              .9866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene 43,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EBV
     δõ
                                                           Query Match
Best Local Similarity
Matches 206; Conserv
1572 tacccctgggagcccatcggagaccccaggccccagcccagcaggacctgcaggggacga 1631
                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                           Conservative
                                                                                                                                                         /gene="H83"
12057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="H80"
9838. 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="H79"
8829. .9866
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TLFALIGDPESRDNMLNFFNGFOTCSPSVGITTCISDNCRKYLPERITYVNNFFVDNI
AGLERNISENTDSFYSNIGFLLYLENPATGITKIIRFPNSLFLFDTILNCLKYFHLK
TGVEEDLLKQMEAYNSKLPFRSSRPTILIRNT"
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PMSHBAFGWQTLSYKIISRLSBQMNSLVFLLWGKHARKLSYLIDAQKHLVLESAHPSP
KVKAARMPFIGCNHFYRTNLFLTEHGKDPINWNILNE"
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//db_xref="01:7687902"
//tanslation="mtnreglsnednygnfqlnksleolrarlvassgevverslskl
kerldyvkdmilknvleadvtvpskclsktkhieokkolvpsdcvrsvpvceikpfi
DMRVFETETTQNARRVRQRTRTTVGSTDGAIGOQRVISGQNRGRARGRGRGRVPRRRN
SNLNNLRTQNSAIVIDDSSETENFENAGSFNEDLLATTILETL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="possible replication protein"
/note="start-codon ggg; similar to HHV6A U80,
spliced in vitro replication protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MYAEERGYGSFDNVIQAYEQIISQSLHLKRFEFDNGCFIEFLAD
SGTCEFFSKGWISMIYWTSETDSMGSLTVDIGKDEGKCRTYRAEGLLLCSKSITSISQ
NTEGERRILTYSHENGKLQITFVTIAKVSSEPELRNLGDLKYMEKFEKECKALDRKH
DDEHRKRSGKQKEKRKVEDIDKKKEDEKLKQEEKKRNDEDKRPDKKDEFDGKYECVAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(11336. .12088)
/gene="H82"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(11336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"similar to HHV6A U81, HCMV UL114, BKRF3, EHV1 61, VZV 59, HSV1 UL2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(10493. .11260)
/gene="H81"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(10493.
/gene="H81"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VNFFIIGVSRSWTFLNSICFVVISEPPKEKRQKSHHETKRNLEEQSHEDGIAPTSTTF
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/db_xref="GI:2769718"
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/transl_except=(pos:9838.
/product="H80"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNGAVEGALSPCVSIDNHEDQQHDELDKRVYAQVGGVLGSPKPRSLESLLCVSKADLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             replication protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="H82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="H80"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAC40328.1"
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/note="similar to HHV6A U79, HCMV UL112,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3829. .9866
/gene="H79"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
                                                                                  4.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .10449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .10449
                                                           0;
                                                                                  Pred No 2.4e-07;
                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .11260)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .12088)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .9840, aa:Met)
                                                                                                               DB 72;
                                                           166;
                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         spliced
                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HCMV UL113,
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EBV
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/PICTED 14 PAA78213.1"

/PICTED 14 PAA78213.1"

/PICTED 14 PAA78213.1"

/PICTED 14 PAA78213.1"

/PICTED 14 PAA782180"

/KIRNS LATION PROSEPTHCSGFHAAHPSLSWLTGSSPWLVLLQAPGGSLFCHDV
/KIRNS LATION PROSEPTHCSGFTAND PROSEPTING 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                576. .842
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576. .842
/gene="DR1"
/note="86.4% identical to D
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YGYTSRHRGERIHLPWPRYWCLELHPDPYRDARSATVWGHRWGWPPTHVRPRSVQDCG
E"
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/gene="DR6"
5025...5336
/gene="DR6"
6512. .7150
/gene="DR7"
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SSRVESPPFSHAASHAVCAEGGRDLPMHGADGDADEGTDGTLLEKGGADEGAGGNAT
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/gene="DR3"
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/gene="DR3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(5023.
/gene="DRHN1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mplparvshalhrlplshywwlllgrhslrhvhsylrlhkglrl
plpwpeQECLhlhpkpykfllrypClTrQphllQGwpaDsslCe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="DRHN1"
/note="ORF unique to HST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(5023. .5532)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HHV-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="BAA78212.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSSACVALS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BAA78215.1"
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                                                                                                                                                                                                                                                                   codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="68.2% identical to"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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8929. .9384
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/gene="Ul"
/note="25.6% identical to Ul gene
HHV-6"
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/function="transforming activity"
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HHV-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="BAA78221.1"
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HTKKYTHTKKYTHKKIHTHKKIHTHKKHHTYKKHFIYALFSQC"
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complement(8292. .8807)
/gene="LJ1"
/note="16.6% identical toLJ1
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/gene="DRHN2"
/note="ORF unique to HST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVETAMVIVTWRDRCYRSGPITARSAVWRTRSPPCGGWAAGHERTLDVFGPG"
complement(7236. .7706)
/gene="DRHN2"
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/db_xref="GI:4995984"
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RHLFDVIAAAADEHDLLTVGGLCQTHAGVSCELLETVRDPWTAVPGVRMTLTVARAQY
RHWPDARRQLALHTAGHPLGPWIVCAVLSRERETQTPSPPIGSGGVTLGNUTPFPGPR
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/codon_start=1
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                                                                                                                                                             US22 gene family"
                                                                                                                                                                                                                                                                                                                                complement(9467. .10768)
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/protein_id="BAA78222.1"
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                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                             /gene="U2"
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                                                                                                                                                                                                                     'note="92% identical
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hes 204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tacccctgggagcccatcggagaccccaggcccagccaggaacctgcaggggacga 1631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCAGCAGAGCCTCCAGCAGGGCCTCCAGCAGGGCCTCCAGCAGAGCCTCCAGCAGAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCCAGCAGGGCCTCCAGCAGAGCCTCCAGCAGAGCTTCCAGCAGAGCCTCCAGCAGGGCC 129126
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95074921
3 (bases
                                                                                                                                                                                                                                                                                                                                                                      Betaherpesvirinae; Roseolovirus.

1 (bases 19696 to 22886)

1 (bases 19696 to 22886)

1 (bases 19696 to 22886)

2 (bases 19696 to 22886)

2 (bases 19696 to 22886)

2 (bases 19696 to 22886)

3 (bases 19696 to 22886)

4 (bases 19696 to 22886)

4 (bases 19696 to 22886)

5 (bases 19696 to 22886)

6 (bases 19696 to 22886)

7 (bases 19696 to 22886)

7 (bases 19696 to 22886)

7 (bases 19696 to 22886)

8 (bases 19696 to 22886)

9 (bases 1
                                                             suggests acquisition of oriLyt b
J. Virol. 69 (1), 589-596 (1995)
                                                                                                                                                                      Stamey, F.R., Dominguez, G., Black, J.B., Pellett, P.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human herpesvirus 6B.
Human herpesvirus 6B
Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF157706 162114 bp DNA VF
Human herpesvirus 6B strain Z29, complete
AF157706 113162 L14772 L16947
AF157706.1 GI:5733510
                                                                                          Pellett, P.E.
Intragenomic linear amplification
of orityt by
                                                                                                                                                                                                                                                                            Virology 195 (2), 521-531 (1993) 93331710
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04; Conservative
                                                                                                                                                                                                                                        (bases 64106 to 84963)
(bases 64106 to 84963; 106012 to 126166)
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LPVTLPLSFFFFFILLILSRIPHRKKMFCRSPFLGISSMSLASAALCPSSCSFSAGRD
LRCDAAVPEWMTAFVRFLVARPLSADDVRDFVSTFAHCRLALSMPVGAELRFATSDM
LGITQAELAKLSRGYGCCPGMDLTVIGVTIFAEVSALVLVGECGEIYAFNGVFDDALY
RLAEDAFGLWRHGLRREFEVYGSKCLMETGASFFGGMSGVDDALAFAVSFDKALVPLP
WPRGAFFFFAVVPRAEKRWRLIPGGGVAVVIGRFFFGRWTLPLLRRQRVLMDQVGRVY
AASLDGGAVVRLSDSFRAFLAMGVRKLFKNHRFPDGHHWTMQLFVTCVHAFVINLPAV
CDLSPHMVEREMSAVSCGASTTVRRDCEDTLRDGDAGVDTS"
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/gene="U3"
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0; Mismatches
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ches 168;
                                                                                              of human herpesvirus transposition
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Direct Submission
Submitted (02-007-1993) Herpesvirus Section, Centers
Submitted Prevention, 1600 Clifton Road, Mailstop
                                                                                                                                                                                                                                                                                                                                                                                                                                       On Aug 16, 1999 this sequence version replaced gi:405170 gi:405156 gi:305397.
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Direct Submission
Submitted (10-JUN-1999) Herpesvirus Section,
Control and Prevention, 1600 Clifton Road, Ma
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9 (bases 1 t
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8 (bases 641)
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Direct Submission
Submitted (26-JUL-1993) Herpesvirus Section, Centers for Disease Submitted (26-JUL-1993) Herpesvirus Section, Centers for Disease Control and Prevention, 1600 Clifton Road, Mailstop G18, Atlanta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human herpesvirus 6B genome sequence: coding content and comparison with human herpesvirus 6A J. Virol. 73 (10), 8040-8052 (1999) 99412318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pellett, P.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pellett, P.E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human beta herpesviruses reveals conserved replication genes and adjacent divergent open reading frames Arch. Virol. 142 (1), 193-204 (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lindquester,G.J., O'Brian,J.J., Anton,E.D., Greenamoyer,C.A., Pellett,P.E. and Dambaugh,T.R.
Genetic content of a 20.9 kb segment of human herpesvirus 6B strain 229 spanning the homologs of human herpesvirus 6A genes U40-57 and containing the origin of DNA replication
Arch. Virol. 142 (1), 103-123 (1997)
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Pellett, P.E.

Restriction endonuclease mapping and molecular cloning of the human herpesvirus 6 variant B strain Z29 genome Arch. Virol. 141 (2), 367-379 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pellett, P.E
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                                                                                                                                                                                                                                             /rpt_
59
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/protein_id="AAD49614.1"
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                                                                                                                                                                                                                                                                                                                                                     /organism="Human herpesvirus
/strain="z29"
                                                                                                                                                                                                        /note="heterogeneous telomeric unit"
/rpt_type=tandem
                                                                                                                                                                                                                                                                                                              /db_xref="taxon:32604"
/note="variant B"
                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                      3988
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Mailstop G18,
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GLAAFYALWRLHLGSRSELSHPVLEWERTELVLTDRRRGWPCTHLLSGSESQRVSSSD
AGDTWNAATEKAAGGKEEAERGGRQQATDRLASPHLTRGRRDCGRSLQGEEPSAAEDF
ARCRPLLDELCGEGGWLPFAFLTASPHYCLILTEGGPVLALDLNDTSLWRIADDLELL
                                                                                                                                                                                         HGAWSSIPLSVPRPDPRVWVPPPHLLFPSPLPSITPVEDEPSARPRCPPGPAEEPSKC
SPCPPCPSPDAPOSAVPRLSALSVPSPSTARVRFSLSSLSSSSSSSSSSSSSSSSSSS
SPSSPVSPSSRSPTISPIRRGLRAKPWVSSGHPVAFPPAPSSAPPFSKRVPSVPSS
ASPSAPCIGRSRPPSAQTA
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GVTEKGRVTTGDVPFSAHPESEEQTDGHHGRQESGHGDQRGGDGRGHRDDGARRHAND
ETEPQQRGEHEDGEQTDSGREEDAQESEVARRDEKGTEQGGSGRSCGRATQTYGGRGE
complement(2723. .3325)
                                                  /gene="DR3"
/evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MPLTARAGHTLHRLPLSHYWWLLLGRHSLRHVHSYLRLRKGLRLPLPHPEQECLHLHPKPYKFLLRYPCLTRQPHLLGGWPADSLMEDPKPYHPSADSKLLPVPLLTTLSAPSMRVSEPTHCSGFHAADPSLSWLTGGSPWLVLLQAPGGSLECHDVPGPLLLTLSAPSMRVSEPTHCSGFHAADPSLSWLTGGSPWLVLLQAPGGSLECHDVFGRLYLLSHSVSLFLKTGLRQCEAIYRAPLWRVRPLPSLWTCRDPDTAFLPKLLARTARR
                                                                                                                                                 .3325)
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/protein_id="AAD49618.1" /db_xref="GI:5733515"

CDS

gene

/translation="MSRVFSCVLRACVCAGLCCWVCMGVICGDCQRWWRRRCARWGRV GPRVLDGGAWRVRSGDGARSVSRTCETERAPSAARSPVYSPPFVLVSSSSSSSCSSAC SSRVPSPPPSPHAASHAVCAEGGRDLPMHGADGDADEGTDGTLLEKGGADEGAGGNAT GCPEDTHGFARSPGDLMGEMNGDLGDEGETGEGGDNGEGE"

gene

PAEINGVYARAVTRKTKRSETIDRLLLSVLPGHGPHASLRSHLRARSALRPPPDPPR /translation="MQKNMKTKKTKKRGRKEGNTPETERRMEPARSRTSAIPSGLRRR SGPSTPLRPGPEVRHAPTWRTASATTADSHRISPPYTPSSRGRHIHTRGARTRTRETS /evidence=not_experimental 3022. .3501 /protein_id="AAD49617.1" /db_xref="GI:5733514" /codon_start=1 /product="B1" /gene="B1" ′gene≖"B2"

gene

CDS

/evidence=not_experimental 3536. .3775

/gene="B2"

codon_start=1

polyA_signal polyA_signal polyA_signal /evidence=not_experimental 3968. .3974 /evidence=not_experimental /note="DR1; B1; B2" /note="DR1; B1; B2"

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/gene="DR /evidence=not_experimental 3983. .3988 evidence=not_experimental 'note="DR1; B1; B2" 'note="DR1; B1; B2"

/note="US22 gene family; transactivator"
join(5027. .5330,6329. .7203) product="DR6" codon_start=1

CDS

gene

polyA_signal

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SOURCE
ORGANISM
                                                                                                                                                        RESULT 13
AF015297
                                                                   KEYWORDS
                                                                                      VERSION
                                                                                                      ACCESSION
                                                                                                                     DEFINITION
                                                                                                                                         FOCUS
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Matches 207
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                                                                                                                                                                                                                                                                                                                      acaagggatgagccagccgagagacccatcggagaccccaggccccgggccggcaggacct
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                                                                                                                                                                                                                              CCAGCAGAGCTTCCAGCAGAGCC
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                                                                                                                                                                                                                                                                                                  CCAGCAGGGCCTCCAGCAGCAGAGCCTCCAGCAGCAGAGCCTCCAGCAGCAGAGCCT
            Human herpesvirus 6 (strain Uganda-1102).
Human herpesvirus 6 (strain Uganda-1102)
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                      Human herpesvirus
AF015297
Betaherpesvirinae; Roseolovirus
                                                                                    AF015297.1
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7349. .7=^
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/codor
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/gene="B4"
/codon_start=1
/product="B4"
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/gene="B4"
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8250. .8711
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SNVTEFARRGLQRDVAYEEDLELPDRRMCGTMVRHLFDVIAAADEHDLLTVGGLCQ
THAGYSCELLETVRDPWTAVFGVRMTLIVARAGVRLWFDDARRQLRLHLXGAGHPLGPU
VCAVLSRERETQTPSPPIGSGGYILGNVPTPGPREVETAMVIVTVAGPLLSFWPDNGK
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/db_xref="GI:5733516"
/translation="MSIRLRVCVGCVYVRVTVSLPAFNPMRNKIGECTQSHTMCLRAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="B3"
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                                                                                    GI:2343282
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Pred. No. 6.2e-07; 
O; Mismatches 176; Indels O; G
                                                                                                                                                                                                                                129178
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                                                                                                                                         27-AUG-1997
                                                                                                                     complete cds.
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1681 gcaggggacgagccagccgagagcccatcggagaccccaggccccagcccggcaggacct 1740

gcaggggacgagccagccgaggagcccatcggagaccccaggccccggcccggcaggacct 1680 CAAGCAAAGCCTCCAGCAGAGCCTCCAGCAGAGCCTCCAGCAGCAGCATT

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2582 CTAGCAGGGCCTCAAGCAAAGCCTCCAGCAGAGCCTCCAGCAGGGATTCTAGCAGAGCCT

Matches

199;

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Mismatches

178;

Indels

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Gaps

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1561 cccaaaggaaggtacccctgggagcccatcggagaccccaggcccaggcccagcaggacct 1620

CCAGCAGAGCCTCCAGCAGGGATTCTAGCAGAGCCTCCAGTAGAGCCTCCAGCAGGGCCT

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Best Local
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Direct Submission
Submitted (21-JUL-1997) Institut fuer Kliniscue ....
Submitted (21-JUL-1997) Institut fuer Kliniscue ....
Virologie, Universitaet Erlangen-Nuernberg, Schlossgarten
Virologie, Universitaet Erlangen-Nuernberg, Schlossgarten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 ... Schiewe, U., Soergel, A., Schiewe, U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Soergel, A., Schiewe, U., Fleckenstein, B. and Neipel, F. Identification of an human herpesvirus-6 transcription unit homologous to the immediate-early 2 gene of human cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 4742)
Soergel, A., Schiewe, U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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Similarity 52.8
99; Conservative
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TTNSNGHQNFKEVSVKNVSGKATSTSPKSKTHHYSSSSDEEGQYKSPVKTIIQSPSPY
CKLKNPSIMDKNSAKNHTASADKNLTDNSPIRSNLNPTAFNKSNSNKSITNSTSNSDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QSDNYNHPTKAQTIPETTKTKKHEATKDNETSTENQVLTPDVISLSYRPSSYKMDIIK
KIYDTDVIPLPKEALTANGSNRDVDIQKYKKAHIRCRSVQKKKERSSQTNKHDENHAS
SRSDLKERKSNENEDKAVTKARDFSKLNPLLSPLPLTPEPAIDFADHTDKFYSTPEFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSGLYCDADITHTOPLSDNTHODPIYSQESRIFTKTIODPRIYAQTHROCTSSASNLQ
SNESGSTQVRFASELPNQLLOPMYTSHNQNANLQNNFTSLPIQPYRDPYRDIESSYRE
SRNTNRGYDYNFRHHPYRPRGGNGKYNYYNPNSKYQOPYKRCFTRTYNRRGGHHRYD
CSDRSADLPYEHYTYPNYEQQNPDPRMNNYKDFTQLTNKFNFESYDYSMAFSTDSTHV
                                                                                                                                                                                                FEYKQIPKKPCNEKNLKEAVYDICCNGLSNNAAIIMYFTRSKKVAQIIKIMQKELMIR
PNITVSEAFKMNHAPPKYYDKDEIKRFIQLQKQGPQELMDKFENNTTHDLFSRHSDVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MEPAKPSGNNMGSNDERMQDYRPDPMMEESIKEILEESLMCDTS
FDDLIIPGLESFGLIIPESSNNIESNNVEEGSDGELKTLAEQKCKQGNDNDVIQSAMK
                                                                                                                                                                                                                                              KRISGAQKTESEVSEPDDLCYRDYVRLKERKVSEKFKIHRGRVATKDFQKLFRNTMRA
                                                                                                                                                                                                                                                                                         RKTQYKDNKQIKSKSDSKHKTTDMSSDYESNRHADVFKNSPEAGEKFPLHNSSPFNTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAB67722.1"
/db_xref="GI:2343283"
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/db_xref="taxon:10370"
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                      4.0%;
                      Score 92.2; DB 72; Pred. No. 6.4e-05;
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                                           Length 4742;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (21-JUL-1997) Institut fuer Klinische und Molekulare
Virologie, Universitaet Erlangen-Nuernberg, Schlossgarten 4,
Erlangen D-91054, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 13965)
Soergel, A., Schiewe, U., Fleckenstein, B. and Neipel, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human herpesvirus 6
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Soergel, A., Schiewe, U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identification of an human herpesvirus-6 transcription homologous to the immediate-early 2 gene of human cytomegalovirus--evidence for an early/late gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; dsDNA viruses, no RNA s
Betaherpesvirinae; Roseolovirus.
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AF015298.1
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                              LSGLYCDADITHTQPLSDNTHQDPIYSQESRIFTKTIQDPRIVAQTHRQCTSSASNLQ
SNESGSTQVRFASELPNQLLQPMYTSHNQNANLQNNFTSLPYQPYRDPYRDIESSYRE
SRNTNNGYDYNFRHHPYRPRGGMGKYNYYNPNSKYQQPYKRCFTRTYNRRGRGHRSYD
                                                                                                                                                                                                                                                                                  /product="10-2 protein"
/product="10-2 protein"
/protein_id="AAB69858.1"
/protein_id="AAB69858.1"
/db_xref="GI:2384715"
/translation="MEPAKPSONMGSNDERMODYRPDPMMEESIKEILEESIMCDTS
FDDLIIPGLESFGLIIPESSNNIESNNVEEGSDGELKTLAEQKCKQGNDNDVIQSAMK
FDDLIIPGLESFGLIIPESSNNIESNNVEEGSDGELKTLAEQKCKQGNDNDVIQSAMK
ASSKASSRASSRNSSRASSRASSRASSRASSRASSRASSRDSSGASSKASRKASSRAS
SRASSRELRQIYCDSNKRQTPPHDTSINTKFEISEIKFRCGEDLNFYKNTAARLQCFN
                                                                                                                                                                                                                                                                                                                                                                                       /gene-"1e2hom"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="Uganda-1102"
/db_xref="taxon:10368"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                         join(1846. .1904,1993. .2186,7868. .12117)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       no RNA stage; Herpesviridae;
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
10241 CCAGCAGAGCCTCCAGC 10257
                                                                                                                                                                                  10121
                                                                                                                                                                                                                                                                                                                                                                10001
                                                                                                                                                                                                                                                                        10061
                                                                                                                                     1861
                                                                                                                                                                                                                                                                                                                                                                                                             1681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1621
                                                                                                                                                                                                                                                                                                                                                                                                                                                     9941 CAAGCAAAGCCTCCAGCAGAGCCTCCAGCAGAGAGCCTCCAGCAGCAGGGATT 10000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1561 cccaaagaaggtacccctgggagcccatcggagaccccaggcccaagcccagcaggacct 1620
                                                                                                                                                                                                                                                                                                       acaagggatgagccagc 1937
                                                                                     CCAGCAGGGATTCTAGCAGAGCCTCCAGCAGGGATTCTAGCAGGGATTCTAGCAGGGCCT
                                                                                                                           gcaggggacgagccagccgagagcccatcggagaccccaggccccagcccggcaggacct
                                                                                                                                                                           CCAGCAGAGCCTCCAGCAGGGATTCTAGCAGGGCCTCAAGCAAAGCCTCCAGCAGAGCCT
                                                                                                                                                                                                          CCAGTAGAGCCTCCAGCAGGGCCTCAAGCAAAGCCTCCAGCAGAGCCTCCAGCAGAGCCT 10120
                                                                                                                                                                                                                                                                                                                                                             CTAGCAGGGCCTCAAGCAAAGCCTCCAGCAGAGCCTCCAGCAGGGATTCTAGCAGAGCCT 10060
                                                                                                                                                                                                                                                                                                                                                                                               gcaggggacgagccagccgagagcccatcggagaccccaggccccagcccggcaggacct 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAGCAGAGCCTCCAGCAGGGATTCTAGCAGAGCCTCCAGTAGAGCCTCCAGCAGGGCCT 9940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PNITVSEAFKMNHAPPKYYDKDEIKRFIQLQKQGPQELWDKFENNTTHDLFSRHSDVK
TMIIYAATPIDFVGAVKTCNKYAKDNPKEIVLRVCSIIDGDNPISIYNPISKEFKSKF
STLSKC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RKTOKKDNKOIKSKSDSKHKTTDMSSDYESNRHADFKNSPEAGEKFPLHNSSPFNTH
EQSNHSENAIDEEQKKAPNITTSHLQGKQNVRLHATKKCKKKRERDDDSDSSIKNECK
KRISGAQKTESEVSEPDDLCYEDYVRLKERKYSEKFKLHRGRVATKDFQKLFRNYMRA
FEYKQIPKKPCNEKNLKEAVYDICCNGLSNNAAIIMYFTRSKKVAQIIKIMQKELMIR
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Pred. No. 4e-05;
0; Mismatches 178;
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JOURNAL MEDLINE REFERENCE REFERENCE AUTHORS TITLE SOURCE ORGANISM ACCESSION VERSION KEYWORDS RESULT 15 HHU13194/c Locus DEFINITION AUTHORS TITLE JOURNAL HHU13194 21191 bp DNA VRL 17-JUN-1995
Human herpesvirus 6 replication origin-binding protein (HDRFO),
partial cds, helicase-primase component (HDRFI), virion protein
(HDLFI), putative helicase (HDRF2), putative phosphoprotein
(EDRF1), replication protein (EDRF2), putative uracil-DNA
glycosylase (EDLF4), putative gL glycoprotein (EDLF3), putative
glycoprotein (EDLF3) genes, complete cds, and major immediate-early Submitted (09-AUG-1994) John Nicholas, Johns Hopkins Oncology Center, Johns Hopkins University, 418 North Bond Street, Balt Nucleotide sequence analysis of a 21-kbp region of the genome human herpesvirus-6 containing homologues of human cytomegalov major immediate-early and replication genes

Virology 204 (2), 738-750 (1994) Direct Submission Human herpesvirus 6. Human herpesvirus 6 Nicholas, J 95027704 U13194.1 GI:862477 protein 2 U13194 Viruses; dsDNA viruses, no RNA s Betaherpesvirinae; Roseolovirus. Nicholas,J. (bases 1 to 21191) (bases 1 to 21191) (BCLFO) gene, no RNA stage; partial cds. Herpesviridae cytomegalovirus Baltimore of

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COMMENT
FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
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Jun 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAA68465.1"
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/protein_id="AAA68465.1"
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TPKNAYALLFDDDLCLLLLQSVFAFLHEKIFGYKQVLVGLCEYIGPDLWPFGNERSV
SFIGYPHLWLLSVSDLERRVPDTYICREILSFCGLAFILGFRGRHAYVPVRELSIEM
PGSETSLQRFRFNSQYVSSESLCFQTGPEDTHLFFSDSDMYVVTLPDCLRLLLKSTVP
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RAFLPCEDENATEIDLLLKFMSRLQHRSYALFDAVIFMLDAFVSAFGRACTLMGMRWIN
RAFLPCEDENATEIDLLLKFMSRLQHRSYALFDAVIFMLDAFVSAFGRACTLMGMRWIN

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HFIEKKITLPGDDMTFQEIISSRETIMNGDFYENGDQLLHKDYITDMGKFRATFLSPG
VDIFIASDIVYDLKNESKRYVFVNVWLQKCVSAGVESTEIERVFCERIKCYMLPKSFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="HDRFO"
3790. .3795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYWIEEFDPNDYCLEYHEGLLDCSRYTAVMSEDGQLVRQARGIALTDKINFSYYILVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"component of helicase-primase complex; similar HCMV UL102 Swiss-Prot Accession Number P16827"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDILQIMQLVFTVHVQFFQXYSLQTLQLFNKLRGMRIVTGVFSIEKFSISILRLFFKC
AFNMTLSASRPRYIPGKAYRNLTKNDMENMLDNWEISRTNLKTCKELRKALTEASRAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FFARLEDKLRWDKKLCLFCSTVLAAEYMYDLIRSRFPLKKVLLLTSKQGKCSSIESWI
RYDVVIYTSVVTVGLSFEPVYFSSLFVYIQLAKGGPDMVSVFQSIGRVRRVIDEDIYI
YMNPVLIRSYDPLAPIAIPPCSDWSVAEQSIISESCIDFRGKCSGAHKYNFCSVLKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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/evidence=not_experimental
complement(3939. .6618)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVRDLHMFYLTCDGKDTHVVMPLLQTAVENCWEKTTEIKQRPTFQCAEISRCGFIVYA
RFFLSSGLSQSKEAHWTVTASKYLSACIRTNKTGLCFASITVYFQDMMCVFIANRYNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="HDRF1"
1949. .3937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1949
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                                                                                                                                                        complement(3939. .3944)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=not_experimental
3790. .3795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RKOTIYKLOGSDISLSVSEVGVFGQHASPGVCVSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="SLHRLTENYDVLILDEIMSIIKQFYSKTMTKTKEVDCKFLSLIK
NSSHVIAMDATLTRHYVEFFAAFKPDTQIALIRNTFVSAMFSNRIAYFCDTFFGKEFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="replication origin-binding protein"
/protein_id="AAA68464.1"
/db_xref="GI:662096"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="HDRF0"
<1. .1980
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/map="109-130 kbp"
/note≖"similar to HH6 CB2L gene product, GenBank Accession
                                                                                                                     /gene="HDLF2"
                                                                                                                                                                                 /gene="HDLF1"
                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="HDRFO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="HDRFO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="HDRF1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene-"HDRF0"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="Ul102"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Human herpesvirus 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
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                            gene
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LHTVVFFYWFYARLYKTPLYEDGIYPCLYCVGSFYQSRALYTSIPLTQNKDWKRGID
VLSALICDDLLSKYCEVDUNNIIFUNUKRCADHAFGDPLKHLEFGLPLKPEBLIKYVG
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TFEDYKSEIGNESLEIEPWFKSNIHRLWTYSOFADODLSKTYOLEEIYUEDGSVEETL
ITCHLKHIRNSSIGYTSKIKASTYGFSGTYKKFVELLOSDLFIEKTSCDOTHAYSFIL
SGLMFGGMYSFCCSKFTTPEVLMEIKNIKMPSIEFLESEMSRMSPDVQTVETDERYDF
GLVNDGLSDVDLLEIDPCGDPFTTRYSKLPLTWSLFSEEISLLYTFYFENDIFIESFAIN
OKHTKGKFGKTLLYTYKRNINYSRYGCEIYSHLKSFYGMLTYAIPANNYTLEGYTNN
VYHLGTDKQLPQILYKKGLPRLVIKDEMGFISVLDNNVSKFIDVVNGOSFHLCTTVDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'translation-"MKSLKKLKELETSDYFNILHVRTILKVIKIDKCISLARHPLVNI
TVGDDGIWFHLEDGTMINGLETKTICEKELGFOGFIGIIILDSEDTLQELELNPFQFK
RRLIHHKVDTPEEFMLGGLVFALENLPLKQSTLHKLIAKLVLFPALSPITKILFNTCD
TLVCTLRHIFFNEHASEILHKVPLMIRLYNEMKNTHIEVLELYFNTKRSHNFINLSLE
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                                                                                                                                                                                                                                                                                                    /evidence-not_expecomplement(10022.
                                                                                                                                                                                                                                                                                                                                                             9404. .9409
/gene="HDRF2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="msisslfggrydnkfllnmssapkielivdkvaslserrlegrl
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LAANLDCIVTATTSIAAQNLSVYLNRSKSAQVKTIFKTFGFNSSHVSMSERQSYIAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="putative helicase; similar to HCMV UL105
Swiss-Prot Accession Number P16736"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IEKEEKSSDAKKSLIKFLLNLSDSKEKIGIRDSVEGFIQEITPSIIDQNKLMLNRGQF
RKRSAIDTGERDVRDLFKKQIIKCMEEGIQTOMDEIETIKTTROMFERRIKDLHSLLE
TNNDCDRYMPINLDHDLENLSLSRALMIVQRLFFTSVSIDDTROVANSFFEQYIPDTQ
ADKRIDQLMEMEYMRTFRLRKNVNNQGQEESITYSNYSIELLIVPFLRRFLNIYNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILGDISNIINFILQSIDNSHYNRYVDWICTVGIVPFMRTTHTAPNLYNLLQQVSSKLI
HDIVRHKQNIVTPVLLGLSSVIIPDFHNIKIFRDRNSEQISCFKNKKAIAFFTYSTPY
VIRNRLMLTTPLAHLSPELKKHNSLRRHQKMCQLLNTFPIKVLTTAKTDVTNKKIMDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MHRASANSLLNSVSGSMMWRNQSSGRRPSKRLSDNEATLSTINS
ILGAEDMLSKNLLSYLPPNNEEIDMIYPSEQIMTFIEMLHGHKNFFKGQTIHNALRDS
AVLKKQIAYGVAQALLNSVSIQQIHDEWKRHVRSFPFHNKKLSFQDYFSVWAHAIKQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(4630. .6618)
/gene="HDLF1"
                                                  YTLSTTA"
                                                                                     /translation="MNMLAYFLYCRQLLLAVVLIEFPPRLCGNTLRFYSYHLPLSTCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LNYENDNFIAPHIVKALKNENTMLIF" complement(9325. .9330)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATVSKVSMTITKSQGLSIQKVAIDFGSDPKNLKLSSIYVGMSRVTDPNNLIMNVNPLF
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/gene="HDRF2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPEEFLFLSLGEILLAIYESSKIKHYLRLVYVRELNQISEVFNLTQTHPENSEPIFDS
NIFSPNPENEILEKIKRIRNLRRIQHLTRPNYPKGDQD"
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/db_xref="GI:662099"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="unknown"
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                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                       gene="EDLF5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="EDLF5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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Search completed: October 12, 2000, 18:53:59 Job time: 38215 sec
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Best Local Sim:
Matches 176;
                                                                                                                                               19191 TCTAGCAGGGCCTCCAGCAGCCTCCAGC 19162
                                                                                                                                                                                                                                                                                                                                                                                 19311 TCCAGCAGAGCCTCCAGCAGAGCCTCCAGCAGGGATTCTAGCAGGGCCTCAAGCAAAGCC 19252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19371 TCTAGCAGAGCCTCCAGTAGAGCCTCCAGCAGGGCCTCAAGCAAAGCCTCCAGCAGAGCC 19312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19431 TCCAGCAGAGCCTCCAGCAGGGATTCTAGCAGAGCCTCCAGCAGAGCCTCCAGCAGGGAT 19372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19491 CCCAGCAGAGCCTCAAGCAGACCTCCAGCAGGGATTCTAGCAGGGCATCAAGCAGAGCC 19432
                                                                                                                                                                                                                                                                      19251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1668 cccggcaggacctgcaggggacgagccagccgagggcccatcggagaccccagggcccag 1727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      y Match 3.7%;
Local Similarity 53.3%;
hes 176; Conservative (
                                                                                                                                                                                 cccggcaggacctacaagggatgagccagc 1937
                                                                                                                                                                                                                                                                                                                                                                                                                cccggcaggacctgcaggggacgagccagccgagagcccatcggagacccccaggcccccg 1847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cccggcaggacctacaagggatgagccagccgagagcccatcggagacccccaggcccccg 1787
                                                                                                                                                                                                                                                                TCCAGCAGAGCCTCCAGCAGGGATTCTAGCAGAGCCTCCAGCAGGGATTCTAGCAGGGAT 19192
                                                                                                                                                                                                                                                                                                     cccggcaggacctgcaggggacgagcccagccgagagccccatcggagaccccaggccccag 1907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12483. .13180
/gene="EDRF2"
<12483. .13079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MYAEERAYGSFDDVMEVYQOIVTESIQLKRLHFGSGCLIEFLGD
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DDEHRRESGKOKEKRKVEDTDKKKDDDRRKGEERKRNDEDKQEDKKEESDGKYKCTVV
VNFYFSCVTVVDFFLNSICFVALSELPKEKRQXFHDMKRNLEEQSHEDGITLTSTTLV
VNFYFSCVTVVDFFLNSICFVALSELPKEKRQXFRYDMKRNLEEQSHEDGITLTSTTLV
NGAYEGALPPCISIDNHEDQQHDELDKRAYAQVGGVSGSPKPRSSGSLLCVSKADLFI
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/note-"putative phosphoprotein; similar to HH6 CB7R,
/note-"putative phosphoprotein; similar to HH6 CB7R,
GenBank Accession Number L14772 and HCMV UL112, Swiss-Prot
Accession Number P16768"
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KECLDNVKDNLIKNECADVTGPSKCLSKTKHIEPKKQIVFSDCVRPVFVCEIKPFIDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"putative phosphoprotein; similar to HCMV UL113, Swiss-Prot Accession Number P17151"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 83.6; DB 72;
Pred. No. 0.00062;
0; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 21191;
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